

Sequence_Listing_R10901_Corrected.txt
SEQUENCE LISTING

<110> O'Donnell, Michael E.
Yurieva, Olga

<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 09/642,218

<151> 2000-08-18

<150> 09/057,416

<151> 1998-04-08

<150> 60/143,202

<151> 1997-04-08

<160> 212

<170> PatentIn Ver. 2.1

<210> 1

<211> 2007

<212> DNA

<213> *Thermus thermophilus*

<400> 1

```
tccgggggtg ggggttcccag gtagaccccg gccctcccg tgagccctt taccagggc 60
gccacctctt ccaggggggc caaggcgtgc aaggagagga acgtccgcac cagccctat 120
actagccttg tgagcgccct ctaccgcgc tccgcccc tcacctcca ggaggtggtg 180
gggcaggagc acgtgaagga gccctcttc aaggccatcc gggaggggag gctcgcccag 240
gectacctct tctccgggccc caggggcgtg ggcaagacca ccacggcgag gctcctcgcc 300
atggcggttg ggtgccaggg ggaagacccc ccttgcgggg tctgccccca ctgccaggcg 360
gtgcagaggg gcgcccaccc ggacgtggtg gacattgacg ccgccagcaa caactccgtg 420
gaggacgtgc gggagctgag ggaaaggatc cacctcgccc cctctctgct ccccaggaag 480
gtcttcatcc tggacgaggc ccacatgctc tccaaaagcg ccttcaacgc cctcctcaag 540
accttgagg agcccccgcc ccacgtcttc ttctcttcg ccaccaccga gcccgagagg 600
atgcccccca ccatcctctc ccgcacccag cacttccgt tccgcgcct caccgaggag 660
gagatcgctt ttaagctccg gcgcctctg gaggcgttg ggcgggaggc ggaggaggag 720
gccctctctc tctcgcccg cctggcggac ggggccctta gggacgcgga aagcctcctg 780
gagcgcttcc tctcctgga aggccccctc acccggaagg aggtggagcg cgccttaggc 840
tccccccag ggaccggggt ggccgagatc gccgcctccc tcgcgagggg gaaaacggcg 900
gaggcccttg gcctcgccc ggcctctac ggggaagggt acgccccgag gagcctggtc 960
tcgggccttt tggaggtgtt ccgggaaggc ctctacgcgc ccttcggcct cgcgggaacc 1020
ccccctcccg cccgccccca ggccctgac cgcgccatga ccgcctgga cgaggccatg 1080
gagcgccctg cccgcgcctc cgacgcctta agcctggagg tggcctcct ggaggcggga 1140
agggccttg ccgcgaggc cctaccccag cccacgggag ctcttcccc agaggtcggc 1200
cccaagccgg aaagcccccc gaccccgga ccccaaggc ccgaggaggc gcccgacctg 1260
cgggagcggt ggcgggcctt cctcgaggcc ctacggcca cctacgggc ctctgtgcg 1320
gaggcccgcc cggaggtccg ggaaggccag ctctgcctcg ctttccccga ggacaaggcc 1380
ttccactacc gcaaggcctc ggaacagaag gtgaggctcc tccccctggc ccaggcccat 1440
ttcggggttg aggaggtcgt cctcgtcctg gaggagaaaa aaaaaagcct gagcccaagg 1500
ccccgcccgg ccccaacctc tgaagcgccc gcacccccgg gccctccga ggaggaggta 1560
```

Sequence_Listing_R10901_Corrected.txt

```

gagggcggagg aagcggcgga ggaggccccg gagggagcct tgaggcggggt ggtccgcctc 1620
ctggggggggc ggggtgctctg ggtgcggcggg cccaggaccc gggaggcgcc ggaggaggaa 1680
cccctgagcc aagacgagat aggggggtact ggtatataat gggggcatga cgcggaccac 1740
cgacctcgga caagagacgg tggacaacat cctcaagcgc ctccgcgta ttgaggggcca 1800
ggtgcggggg ctccagaaga tgggtggccga gggccgcccc tgcgacgagg tctcaccaca 1860
gatgaccgcc accaagaagg ccatggaggc ggcggccacc ctgatcctcc acgagttcct 1920
gaacgtctgc gccgcgagg tctccgagg caaggtgaac cccaagaagc ccgaggagat 1980
cgccaccatg ctgaagaact tcattcta 2007

```

<210> 2

<211> 529

<212> PRT

<213> *Thermus thermophilus*

<400> 2

```

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1           5           10           15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
          20           25           30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
          35           40           45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
          50           55           60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
          65           70           75           80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
          85           90           95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
          100          105          110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
          115          120          125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
          130          135          140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
          145          150          155          160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
          165          170          175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
          180          185          190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
          195          200          205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
          210          215          220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro

```

Sequence_Listing_R10901_Corrected.txt

```

225                230                235                240
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
      245                250                255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
      260                265                270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
      275                280                285
Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
      290                295                300
Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
      305                310                315                320
Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
      325                330                335
Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
      340                345                350
Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
      355                360                365
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
      370                375                380
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
      385                390                395                400
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
      405                410                415
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
      420                425                430
Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
      435                440                445
Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
      450                455                460
Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu
      465                470                475                480
Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
      485                490                495
Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
      500                505                510
Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Gly Thr Gly
      515                520                525
Ile

```

Sequence_Listing_R10901_Corrected.txt

<210> 3
 <211> 1590
 <212> DNA
 <213> Thermus thermophilus

```

<400> 3
gtgagcgccc tctaccgccc ctcccgcccc ctcaccttcc aggaggtggt ggggcaggag 60
caagtgaagg agccccctct caaggccatc cgggagggga ggctcgccca ggccctacctc 120
ttctccgggc ccaggggcgt gggcaagacc accacggcga ggctcctcgc catggcggtg 180
gggtgccagg gggaagaccc ccttgcggg gtctgcccc actgccaggc ggtgcagagg 240
ggcgccccc ccgaagtggt ggacattgac gccgccagca acaactccgt ggaggacgtg 300
cgggagctga gggaaaggat ccacctcgcc cccctctctg cccccaggaa ggtcttcctc 360
ctggacgagg ccacatgct ctccaaaagc gccttcaacg cctcctcaa gaccctggag 420
gagccccgcg ccacgctcct ctctgtcttc gccaccacgc agcccgagag gatgcccccc 480
accatcctct cccgcaccca gcacttcgcg ttccgcccgc tcacggagga ggagatcgcc 540
tttaagctcc ggcgcctcct ggaggccgtg gggcgggagg cggaggagga ggccctcctc 600
ctcctcgccc gcctggcgga cggggccctt agggacgcgg aaagcctcct ggagcgcttc 660
ctcctcctgg aaggccccct cacccggaag gaggtgagc gcgcctagg ctccccccca 720
gggaaccggg tggccgagat cgccgcctcc ctgcgcaggg ggaaaacggc ggaggccctg 780
ggcctcgccc ggcgcctcta cggggaaggg tacgccccga ggagcctggt ctcgggcctt 840
ttggaggtgt tccgggaagg cctctacgcc gccttcggcc tcgcgggaac ccccttccc 900
gccccgcccc aggcctgat cgccgccatg accgccttg acgaggccat ggagcgctc 960
gcccgcgct ccgaagcctt aagcctggag gtggccctcc tggaggcggg aagggcctg 1020
gccgcccagg cctaccccc gcccacgggc gctccttccc cagaggtcgg cccaagccg 1080
gaaagcccc cgaccccgga acccccaagg cccgaggagg cggccgacct gcgggagcgg 1140
tggcgggcct tctcgaggc cctcaggccc accctacggg ccttcgtgcg ggaggccgc 1200
ccggaggtcc gggaaggcca gctctgcctc gctttcccc aggacaaggc cttccactac 1260
cgcaaggcct cggaacagaa ggtgaggtc ctcctccttg cccaggccca ttctggggtg 1320
gaggaggtcg tctcgtcct ggaggagaa aaaaaaagcc tgagcccaag gcccgcgccg 1380
gccccacctc ctgaagcgcc cgcaccccc ggccctccc aggaggaggt agaggcggag 1440
gaagcgcgcg aggaggcccc ggaggaggcc ttgaggcggg tggtcgcct cctggggggg 1500
cgggtgctct gggtgcgcg gcccaggacc cgggaggcgc cggaggagga acccctgagc 1560
caagacgaga taggggttac tggtatataa 1590
    
```

<210> 4
 <211> 464
 <212> PRT
 <213> Thermus thermophilus

```

<400> 4
Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1             5             10             15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20             25             30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35             40             45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50             55             60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65             70             75             80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85             90             95
    
```

Sequence_Listing_R10901_Corrected.txt

```

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
    100                      105                      110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
    115                      120                      125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
    130                      135                      140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
    145                      150                      155                      160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
    165                      170                      175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
    180                      185                      190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
    195                      200                      205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
    210                      215                      220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
    225                      230                      235                      240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
    245                      250                      255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
    260                      265                      270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
    275                      280                      285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
    290                      295                      300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
    305                      310                      315                      320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
    325                      330                      335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
    340                      345                      350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
    355                      360                      365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
    370                      375                      380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
    385                      390                      395                      400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys

```

Sequence_Listing_R10901_Corrected.txt

405

410

415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430
 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445
 Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser
 450 455 460

<210> 5

<211> 454

<212> PRT

<213> Thermus thermophilus

<400> 5

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15
 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30
 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45
 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60
 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80
 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95
 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
 100 105 110
 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
 115 120 125
 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Pro Pro Pro
 130 135 140
 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
 145 150 155 160
 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
 165 170 175
 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
 180 185 190
 Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
 195 200 205

Sequence_Listing_R10901_Corrected.txt

```

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
 210                215                220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
225                230                235                240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
                245                250                255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
                260                265                270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
                275                280                285

Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
290                295                300

Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
305                310                315                320

Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
                325                330                335

Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
                340                345                350

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
                355                360                365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
                370                375                380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
385                390                395                400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
                405                410                415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
                420                425                430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
                435                440                445

Gly Glu Lys Lys Lys Ala
450

```

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

Sequence_Listing_R10901_Corrected.txt 32
cgcaagcttc acgcstacct sttctccggs ac

<210> 7
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 7
His Ala Tyr Leu Phe Ser Gly Thr
1 5

<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 8
cgcgattcg tgctcsggsg gctcctcsag sgtc 34

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 9
Lys Thr Leu Glu Glu Pro Pro Glu His
1 5

<210> 10
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 10
gcgcggatcc ggagggagaa aaaaaaagcc tcagccca 38

<210> 11
<211> 38
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

gcgcggatcc ggagggagag aagaaaagcc tcagccca

38

<210> 12

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

gaattaaatt cgcgcttcgg gaggtggg

28

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 13

gcgcgaattc gcgcttcggg aggtggg

27

<210> 14

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 14

gcgcgaattc gggcgcttca ggaggtggg

29

<210> 15

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 15

gtggtgcata tggtagcgc cctctaccgc c

31

<210> 16

<211> 31

<212> DNA

<213> Artificial Sequence

Sequence_Listing_R10901_Corrected.txt

<220>

<223> Description of Artificial Sequence: primer

<400> 16

gtgggtggtcg acccaggagg gccacctcca g

31

<210> 17

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> PEPTIDE

<222> (2)

<223> X is any aa at position 2

<220>

<221> PEPTIDE

<222> (3)

<223> X is any aa at position 3

<220>

<221> PEPTIDE

<222> (5)

<223> X is any aa at position 5

<400> 17

Gly Xaa Xaa Gly Xaa Gly Lys Thr
1 5

<210> 18

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 18

Lys Pro Asp Pro Lys Ala Pro Pro Gly Pro Thr Ser
1 5 10

<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Sequence_Listing_R10901_Corrected.txt

```

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
   35                               40                               45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
   50                               55                               60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
   65                               70                               75                               80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
   85                               90                               95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
  100                               105                               110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
  115                               120                               125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
  130                               135                               140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
  145                               150                               155                               160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
  165                               170                               175

Ala Leu Asp Val
  180

```

<210> 20

<211> 180

<212> PRT

<213> Bacillus subtilis

<400> 20

```

Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
   1                               5                               10                               15

Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
  20                               25                               30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
  35                               40                               45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
  50                               55                               60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
  65                               70                               75                               80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
  85                               90                               95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
  100                               105                               110

```

Sequence_Listing_R10901_Corrected.txt

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
165 170 175

Arg Ile Thr Ser
180

<210> 21

<211> 294

<212> PRT

<213> Escherichia coli

<400> 21

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn
180 185 190

Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg

195 200 205

```
<210> 22
<211> 294
<212> PRT
<213> Haemophilus influenzae
```

```

<400> 22
Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
  1          5          10          15
Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
          20          25          30
Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
          35          40          45
Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
          50          55          60
Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
          65          70          75          80
Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
          85          90          95
Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
          100          105          110
Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
          115          120          125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
          130          135          140
Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
          145          150          155          160
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
          165          170          175

```

Sequence_Listing_R10901_Corrected.txt

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
 180 185 190
 Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
 195 200 205
 Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
 210 215 220
 Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
 225 230 235 240
 Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
 245 250 255
 His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
 260 265 270
 Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
 275 280 285
 Leu His Gln Ile Ala Leu
 290

<210> 23
 <211> 294
 <212> PRT
 <213> Bacillus subtilis

<400> 23
 Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
 1 5 10 15
 Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
 20 25 30
 Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
 35 40 45
 Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
 50 55 60
 Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
 65 70 75 80
 Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
 85 90 95
 Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
 100 105 110
 Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
 115 120 125
 His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
 130 135 140

Sequence_Listing_R10901_Corrected.txt

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
 145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
 165 170 175

Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp
 180 185 190

Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser
 195 200 205

Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala
 210 215 220

Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile
 225 230 235 240

Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu
 245 250 255

His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu
 260 265 270

Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr
 275 280 285

Phe Arg Asp Met Leu Leu
 290

<210> 24

<211> 300

<212> PRT

<213> *Caulobacter crescentus*

<400> 24

Asp Ala Tyr Thr Val Leu Ala Arg Lys Tyr Arg Pro Arg Thr Phe Glu
 1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
 20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
 35 40 45

Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
 50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
 65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
 85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
 100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile

Sequence_Listing_R10901_Corrected.txt

115

120

125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
1 5 10 15

Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Sequence_Listing_R10901_Corrected.txt

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100 105 110
His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115 120 125
Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130 135 140
Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys
145 150 155 160
Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
165 170 175
Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
180 185 190
Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
195 200 205
Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
210 215 220
Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
225 230 235 240
Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
245 250 255
Tyr Gln Glu Ile
260

<210> 26
<211> 289
<212> PRT
<213> Thermus thermophilus

<400> 26
Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
1 5 10 15
Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
20 25 30
Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
35 40 45
Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50 55 60
Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65 70 75 80
Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85 90 95

Sequence_Listing_R10901_Corrected.txt

```

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
    100                      105                      110

Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
    115                      120                      125

Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
    130                      135                      140

His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
    145                      150                      155                      160

Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
    165                      170                      175

Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
    180                      185                      190

Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
    195                      200                      205

Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
    210                      215                      220

Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
    225                      230                      235                      240

Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
    245                      250                      255

Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
    260                      265                      270

Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
    275                      280                      285

```

Tyr

<210> 27

<211> 101

<212> RNA

<213> Thermus thermophilus

<400> 27

```

guccuggagg gagaaaaaaa aagccugagc ccaaggcccc gcccgcccc accuccugaa 60
gogcccgcac ccccgggccc ucccgaggag gagguagagg c 101

```

<210> 28

<211> 11

<212> PRT

<213> Thermus thermophilus

<400> 28

```

Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
    1                      5                      10

```

<210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> unsure
 <222> (6)
 <223> N at position 6 is either G or C

<220>
 <221> unsure
 <222> (12)
 <223> N at position 12 is either G or C

<220>
 <221> unsure
 <222> (21)
 <223> N at position 21 is either G or C

<400> 29
 cacgcntacc tnttctccgg nac

23

<210> 30
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<220>
 <221> unsure
 <222> (7)
 <223> N at position 7 is either G or C

<220>
 <221> unsure
 <222> (10)
 <223> N at position 10 is either G or C

<220>
 <221> unsure
 <222> (19)
 <223> N at position 19 is either G or C

<220>
 <221> unsure
 <222> (22)
 <223> N at position 22 is either G or C

<400> 30
 gtgctenggn ggctcctcnt cngtc

25

Sequence_Listing_R10901_Corrected.txt

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa 33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggscststcs gagcagaag 29

<210> 33
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 33
gcgggatcct caacgaggac ctctccatct tcaa 34

<210> 34
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 34
gcgggatcct tgtcgtsag sgtsagsgcg tcgta 35

<210> 35
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 35
gggaaggacc agcgcgtact cccctgctc ctaggtgtg 39

Sequence_Listing_R10901_Corrected.txt

```

<210> 36
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 36
gtgtggatcc ttctttcttsc ccatsgc                27

<210> 37
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 37
caccgattcc agtgggtgcct aggtgtg                27

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 38
caacacctgg tgttccagga gcctgtgctt            30

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 39
ccagaatcgt ctgctggtcg tag                    23

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  primer

<400> 40

```

agcaccctgg aggagcttc

19

<210> 41
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (7)
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (13)
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> (14)
<223> N at position 14 is A, C, G, or T

<400> 42
gtsgtsnnsq acnnsagagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

Sequence_Listing_R10901_Corrected.txt

```

<220>
<221> unsure
<222> (9)
<223> N at position 9 is A, C, G, or T

<220>
<221> unsure
<222> (17)
<223> N at position 17 is A, C, G, or T

<220>
<221> unsure
<222> (18)
<223> N at position 18 is A, C, G, or T

<400> 43
gaasccsnng tcgaasnngg cgttgtg 27

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 44
cggggatcca cctcaatcac ctctgtg 27

<210> 45
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 45
cggggatccg ccaccttgcg gctccgggtg 30

<210> 46
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 46
gcgctctaga cgagttccca aagcgtgcgg t 31

<210> 47
<211> 25
<212> DNA

```

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 47
cgcgctctaga tcacctgtat ccaga 25

<210> 48
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 48
gcggcgccata tgggtggtggt cctggacctg gag 33

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 49
cgcgctctaga tcacctgtat ccaga 25

<210> 50
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 50
gtscstsgtsa agacscactt 20

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 51
sagsagsgcg ttgaasgtgt g 21

<210> 52
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 52
ctcgttggtg aaagtttcg tg 22

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 53
cgtccagttc atcgccggaa agga 24

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 54
tctggcaaca cgttctggag cacatcc 27

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 55
tgctggcggt catcttcagg atg 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 56
catcctgaag atgaacgcca gca 23

<210> 57

```

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 57
agggttatcca caggggtcat gtgca                25

<210> 58
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 58
gtgtgtcata tgaacataac ggttcccaa            29

<210> 59
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 59
gcgcgaattc tcccttgtgg aaggcttag            29

<210> 60
<211> 13
<212> PRT
<213> Thermus thermophilus

<400> 60
Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
 1             5             10

<210> 61
<211> 14
<212> PRT
<213> Thermus thermophilus

<400> 61
Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
 1             5             10

<210> 62
<211> 8
<212> PRT
<213> Thermus thermophilus

```

<400> 62

Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63

<211> 8

<212> PRT

<213> Thermus thermophilus

<400> 63

Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64

<211> 6

<212> PRT

<213> Thermus thermophilus

<400> 64

Ala Met Gly Lys Lys Lys
1 5

<210> 65

<211> 9

<212> PRT

<213> Thermus thermophilus

<400> 65

Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<220>

<221> PEPTIDE

<222> (3)

<223> Xaa at position 3 is undefined

<220>

<221> PEPTIDE

<222> (5)

<223> Xaa at position 5 is undefined

<400> 66

Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 67
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <221> PEPTIDE
 <222> (4)
 <223> Xaa at position 4 is undefined

<220>
 <221> PEPTIDE
 <222> (7)
 <223> Xaa at position 7 is undefined

<400> 67
 His Asn Ala Xaa Phe Asp Xaa Gly Phe
 1 5

<210> 68
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<220>
 <221> PEPTIDE
 <222> (3)
 <223> Xaa at position 3 is undefined

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at position 5 is undefined

<400> 68
 Val Val Xaa Asp Xaa Glu Thr Thr Gly
 1 5

<210> 69
 <211> 7
 <212> PRT
 <213> Thermus thermophilus

<400> 69
 Val Leu Val Lys Thr His Leu
 1 5

<210> 70
 <211> 6
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 70

His Arg Ala Leu Tyr Asp
1 5

<210> 71

<211> 7

<212> PRT

<213> *Thermus thermophilus*

<400> 71

His Thr Phe Asn Ala Leu Leu
1 5

<210> 72

<211> 34

<212> PRT

<213> *Escherichia coli*

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro
20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> *Vibrio cholerae*

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu
1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro
20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> *Haemophilus influenzae*

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu

Sequence_Listing_R10901_Corrected.txt

1 5 10 15
Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro
 20 25 30

Leu Val

<210> 75
<211> 34
<212> PRT
<213> Rickettsia prowazekii

<400> 75
Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 5 10 15
Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
 20 25 30

Ile Val

<210> 76
<211> 34
<212> PRT
<213> Helicobacter pylori

<400> 76
Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15
Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
 20 25 30

Ile Ile

<210> 77
<211> 34
<212> PRT
<213> Synechocystis sp.

<400> 77
Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15
Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
 20 25 30

Ile Val

<210> 78
<211> 34

Sequence_Listing_R10901_Corrected.txt

<212> PRT

<213> Mycobacterium tuberculosis

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp

35

40

45

<210> 82

<211> 46

<212> PRT

<213> *Rickettsia prowazekii*

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp
 1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys
 20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp
 35 40 45

<210> 83

<211> 45

<212> PRT

<213> *Helicobacter pylori*

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser
 1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp
 20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln
 35 40 45

<210> 84

<211> 46

<212> PRT

<213> *Synechocystis* sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
 1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
 20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
 35 40 45

<210> 85

<211> 46

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
 1 5 10 15

Sequence_Listing_R10901_Corrected.txt

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

```

atgggcccggg agctccgctt cgcccacctc caccagcaca cccagttctc cctcctggac 60
ggggcggcga agctttccga cctcctcaag tgggtcaagg agacgacccc cgaggacccc 120
gccttgccca tgaccgacca cggcaacctc ttccggggccg tggagttcta caagaaggcc 180
accgaaatgg gcatcaagcc catcctgggc tacgaggcct acgtggcggc ggaaagccgc 240
tttgaccgca agcggggaaa gggcctagac gggggctact ttacctcac cctcctcgcc 300
aaggacttca cgggggtacca gaacctggtg cgcttgccga gccgggctta cctggagggg 360
ttttacgaaa agccccgat tgaccgggag atcctgcgcg agcacgccga gggcctcatc 420
gcctctctcg ggtgcctcgg ggcggagatc cccagttca tcctccagga ccgtctggac 480
ctggccgagg cccggctcaa cgagtacctc tccatcttca aggaccgctt cttcatcgag 540
atccagaacc acggcctccc cgagcagaaa aaggtcaacg aggtcctcaa ggagttcgcc 600
cgaaagtacg gcttggggat ggtggccacc aacgacggcc attacgtgag gaaggaggac 660
gcgcgcgccc acgaggtcct cctcgccatc cagtccaaga gcacctgga cgacccggg 720
cgctggcgct tccccgcca cgagttctac gtgaagaccc ccgaggagat gcgggccatg 780
ttccccgagg aggagtgggg ggacgagccc ttgacaaca ccgtggagat cgcccgcatg 840
tgcaacgtgg agctgcccac cggggacaag atggtctacc gaatcccccg cttccccctc 900
cccgaggggc ggaccgaggc ccagtacctc atggagctca cttcaaggg gctcctccgc 960
cgctaccggg accggatcac cgagggttc tacggggagg tcttcgcct tttggggaag 1020
cttccccccc acggggacgg ggaggccttg gccgaggcct tggcccaggt ggagcgggag 1080
gcttgggaga ggctcatgaa gagcctcccc cctttggccg ggtcaaggga gtggacggcg 1140
gaggccattt tccaccgggc cctttacggg ctttcctgga tagagcgcat ggggtttccc 1200
ggctacttcc tcatcgcca ggactacatc aactgggccc ggagaaacgg cgtctccgtg 1260
gggcccggca gggggagcgc cgcgggagc ctggtggcct acgcctgagg gatcaccac 1320
attgaccccc tccgcttcgg cctcctcttt gagcgcttcc tgaacccgga gagggtctcc 1380
atgcccagca ttgacacgga cttctccgac cgggagcggg accgggtgat ccagtacgtg 1440
cgggagcgct acggcgagga caaggtggcc cagatcgcca ccctgggaag cctcgccctc 1500
aaggccgccc tcaaggacgt ggcccgggtc tacggcatcc cccacaagaa ggccggaggaa 1560
ttggccaagc tcatcccggg gcagttcggg aagcccaagc cctgcagga ggccatccag 1620
gtggtgccgg agcttagggc ggagatggag aaggaccca aggtgcggga ggtcctcgag 1680
gtggccatgc gcctggaggg cctgaaccgc cagcctccg tccacgcgcg cggggtggtg 1740
atcgccgcgc agccctcac ggacctcgtc cccctcatgc gcgaccagga agggcgggcc 1800
gtcaccacgt acgacatggg ggcggtggag gccttggggc ttttgaagat ggactttttg 1860
ggcctccgca cctcacctt cctggacgag gtcaagcga tcgtcaaggc gtcccagggg 1920
gtggagctgg actacgatgc cctccccctg gacgaccca agaccttcgc cctcctctcc 1980
cggggggaga ccaagggggg cttccagctg gagtccgggg ggatgaccgc cagctccgc 2040
ggcctcaagc cgcggcgtt tgaggacctg atcgccatcc tctcctcta ccgccccggg 2100
cccatggagc acatccccac ctacatccgc cgccaccaag ggtggagcc cgtgagctac 2160
agcgagtttc ccacgcgga gaagtaccta aagcccatcc tggacgagac ctacggcatc 2220
ccgtctacc aggagcagat catgcagatc gcctcggcgc tggcggggta ctcctgggc 2280
gaggcggacc tctgcgggc gtccatgggc aagaagaagg tggaggagat gaagtccac 2340
cgggagcgct tcgtccaggg ggccaaggaa agggcggtgc ccgaggagga ggccaaccgc 2400
ctctttgaca tgctggaggc cttcgccaac tacggttca acaaatccca cgtgcgcgc 2460
tacagcctcc tctcctacca gaccgctac gtgaaggccc actacccgt ggagttcatg 2520
gccgcctccc tctcgttga ggggaacgac tccgacaagg tggccgagta catccgcac 2580
gcccgggcca tgggcataga ggtccttccc ccgagctca accgtccgc gtttgacttc 2640
ctgggtccagg gccggcagat ccttttcggc ctctccgcgc tgaagaacgt gggcgaggcg 2700

```

Sequence_Listing_R10901_Corrected.txt

```

ggggcggagg ccattctccg ggagcgggag cggggcggcc cctaccggag cctcggcgac 2760
ttctctcaagc ggctggacga gaaggtgctc aacaagcggg cctcggagtc cctcatcaag 2820
gcgggcgccc tggacggctt cggggaaaagg gcgcgggctcc tcgcctccct ggaagggctc 2880
ctcaagtggg cggccgagaa cggggagaag gcccgctcgg gcatgatggg cctcttcagc 2940
gaagtggagg agccgccttt ggccgaggcc gccccctgg acgagatcac ccggctccgc 3000
tacgagaagg aggccttggg gatctacgtc tccggccacc ccatcttgcg gtaccccggg 3060
ctccgggaga cggccacctg caccctggag gagcttcccc acctggcccg ggacctgccc 3120
ccccggtcta gggctcctct tgccgggatg gtggaggagg tggcgcgcaa gccacaaaag 3180
agcggcggga tgatggcccc cttcgtcctc tccgacgaga cggggcgct tgaggcggtg 3240
gcattcggcc gggcctacga ccaggtctcc ccgaggctca aggaggacac ccccgctgctc 3300
gtcctgcggg aggtggagcg ggaggagggg ggcgtgcggg tgctggccca ggcggtttgg 3360
acctacgagg agctggagca ggtcccccgg gccctcgagg tggagggtga ggcctccctc 3420
ctggacgacc ggggggtggc ccacctgaaa agcctcctgg acgagcacgc ggggaccctc 3480
cccctgtacg tccgggtcca gggcgcttc ggcgaggccc tcctcgccct gagggaggtg 3540
cgggtggggg aggaggctgt aggcggccgc gtggttcggg gcctacctcc tgcccgaccg 3600
ggaggctcct ctccagggcg gccaggcggg ggaggcccag gaggcggtgc ccttctaggg 3660
ggtgggcccgt gagacctagc gccatcgctt tcgcccgggg caaggaggcc tgggcccgcac 3720
cccttttgg 3729

```

<210> 87

<211> 1245

<212> PRT

<213> Thermus thermophilus

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Sequence_Listing_R10901_Corrected.txt

```

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
    180                      185                      190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
    195                      200                      205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His
    210                      215                      220

Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly
    225                      230                      235                      240

Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu
    245                      250                      255

Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu
    260                      265                      270

Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly
    275                      280                      285

Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg
    290                      295                      300

Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg
    305                      310                      315                      320

Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg
    325                      330                      335

Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu
    340                      345                      350

Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser
    355                      360                      365

Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe
    370                      375                      380

His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro
    385                      390                      395                      400

Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys
    405                      410                      415

Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val
    420                      425                      430

Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu
    435                      440                      445

Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile
    450                      455                      460

Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val
    465                      470                      475                      480

Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly
    485                      490                      495

```

Sequence_Listing_R10901_Corrected.txt

```

Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly
500                               505                               510

Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln
515                               520                               525

Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu
530                               535                               540

Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu
545                               550                               555                               560

Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala
565                               570                               575

Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu
580                               585                               590

Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala
595                               600                               605

Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr
610                               615                               620

Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly
625                               630                               635                               640

Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe
645                               650                               655

Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser
660                               665                               670

Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu
675                               680                               685

Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His
690                               695                               700

Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr
705                               710                               715                               720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu
725                               730                               735

Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser
740                               745                               750

Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser
755                               760                               765

Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe
770                               775                               780

Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Glu Ala Asn Arg
785                               790                               795                               800

Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser

```

Sequence_Listing_R10901_Corrected.txt

```

      805                               810                               815
His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys
      820                               825                               830

Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg
      835                               840                               845

His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met
      850                               855                               860

Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe
      865                               870                               875                               880

Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn
      885                               890                               895

Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly
      900                               905                               910

Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys
      915                               920                               925

Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu
      930                               935                               940

Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu
      945                               950                               955                               960

Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met
      965                               970                               975

Gly Leu Phe Ser Glu Val Glu Glu Pro Pro Leu Ala Glu Ala Ala Pro
      980                               985                               990

Leu Asp Glu Ile Thr Arg Leu Arg Tyr Glu Lys Glu Ala Leu Gly Ile
      995                               1000                               1005

Tyr Val Ser Gly His Pro Ile Leu Arg Tyr Pro Gly Leu Arg Glu Thr
      1010                               1015                               1020

Ala Thr Cys Thr Leu Glu Glu Leu Pro His Leu Ala Arg Asp Leu Pro
      1025                               1030                               1035                               1040

Pro Arg Ser Arg Val Leu Leu Ala Gly Met Val Glu Glu Val Val Arg
      1045                               1050                               1055

Lys Pro Thr Lys Ser Gly Gly Met Met Ala Arg Phe Val Leu Ser Asp
      1060                               1065                               1070

Glu Thr Gly Ala Leu Glu Ala Val Ala Phe Gly Arg Ala Tyr Asp Gln
      1075                               1080                               1085

Val Ser Pro Arg Leu Lys Glu Asp Thr Pro Val Leu Val Leu Ala Glu
      1090                               1095                               1100

Val Glu Arg Glu Glu Gly Gly Val Arg Val Leu Ala Gln Ala Val Trp
      1105                               1110                               1115                               1120

```

Sequence_Listing_R10901_Corrected.txt

Thr Tyr Gln Glu Leu Glu Gln Val Pro Arg Ala Leu Glu Val Glu Val
1125 1130 1135

Glu Ala Ser Leu Pro Asp Asp Arg Gly Val Ala His Leu Lys Ser Leu
1140 1145 1150

Leu Asp Glu His Ala Gly Thr Leu Pro Leu Tyr Val Arg Val Gln Gly
1155 1160 1165

Ala Phe Gly Glu Ala Leu Leu Ala Leu Arg Glu Val Arg Val Gly Glu
1170 1175 1180

Glu Ala Leu Gly Ala Leu Glu Ala Ala Gly Phe Pro Ala Tyr Leu Leu
1185 1190 1195 1200

Pro Asn Arg Glu Val Ser Pro Arg Leu Thr Gly Ser Gly Gly Pro Arg
1205 1210 1215

Gly Arg Ala Leu Ser Thr Gly Leu Ala Leu Lys Thr Tyr Pro Ile Ala
1220 1225 1230

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
1235 1240 1245

<210> 88

<211> 198

<212> PRT

<213> Thermus thermophilus

<400> 88

Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
1 5 10 15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu

Sequence_Listing_R10901_Corrected.txt

```

145          150          155          160
Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
          165          170          175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
          180          185          190

Tyr Met Leu Thr Ser Gly
          195

```

```

<210> 89
<211> 182
<212> PRT
<213> Deinococcus radiodurans

```

```

<220>
<221> PEPTIDE
<222> (79)
<223> X at position 79 is undefined

```

```

<400> 89
Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1          5          10          15

Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
          20          25          30

Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
          35          40          45

Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
          50          55          60

Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
          65          70          75          80

Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
          85          90          95

Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
          100          105          110

Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
          115          120          125

Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
          130          135          140

Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
          145          150          155          160

Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
          165          170          175

Glu Leu Leu Gly Glu Arg
          180

```

Sequence_Listing_R10901_Corrected.txt

<210> 90

<211> 201

<212> PRT

<213> Bacillus subtilis

<400> 90

His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
1 5 10 15

Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
20 25 30

Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
35 40 45

Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
50 55 60

Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
65 70 75 80

Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
85 90 95

Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
100 105 110

Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
115 120 125

Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
130 135 140

Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
145 150 155 160

His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
165 170 175

His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
180 185 190

Lys Met Leu Lys Asp Ala Ala Glu Lys
195 200

<210> 91

<211> 188

<212> PRT

<213> Haemophilus influenzae

<220>

<221> PEPTIDE

<222> (47)

<223> X at position 47 is undefined

<220>

<221> PEPTIDE

Sequence_Listing_R10901_Corrected.txt

<222> (57)

<223> X at position 57 is undefined

<400> 91

```

Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
 1             5             10             15

Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
      20             25             30

Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
      35             40             45

Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
      50             55             60

His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
      65             70             75             80

Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
      85             90             95

His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
      100            105            110

Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
      115            120            125

Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
      130            135            140

Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
      145            150            155            160

Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
      165            170            175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
      180            185

```

<210> 92

<211> 189

<212> PRT

<213> Escherichia coli

<400> 92

```

Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
 1             5             10             15

Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
      20             25             30

Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
      35             40             45

His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
      50             55             60

```

Sequence_Listing_R10901_Corrected.txt

```

His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65          70          75          80
Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
          85          90          95
His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
          100          105          110
Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
          115          120          125
Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
          130          135          140
Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
145          150          155          160
His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
          165          170          175
Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
          180          185

```

<210> 93

<211> 201

<212> PRT

<213> Helicobacter pylori

<400> 93

```

Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser
 1          5          10          15
Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
          20          25          30
Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
          35          40          45
His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
          50          55          60
Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
65          70          75          80
Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
          85          90          95
Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
          100          105          110
Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
          115          120          125
Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
          130          135          140
Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu

```

Sequence_Listing_R10901_Corrected.txt

145 150 155 160

Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
 165 170 175

Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
 180 185 190

Leu Asn Leu Pro Ser Tyr Ile Lys Thr
 195 200

<210> 94

<211> 630

<212> DNA

<213> Thermus thermophilus

<400> 94

atggtggagc ggggtggtgcg gacccttctg gacgggaggt tcctcctgga ggaggggggtg 60
gggctttggg agtggcgcta cccctttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
gaggggggga ggcgcctccc cttccagagc ctcgctccgc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catcccccg gaggccctgg aggaggcccc ctccctggag 300
gaggtttctg agaaggcta cccctccgc gccgacgcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttcc cgcgccgcc ttggaggggc tgggctaccg cctggaaaac 420
cccgtggtgg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
ctggacgccc tctccgaggt cctggagctt ccccgaagga cctgccaccg ggcctcag 540
gacgtggagc gcacctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttgggaact cgggaggtag 630

<210> 95

<211> 210

<212> PRT

<213> Thermus thermophilus

<400> 95

Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
1 5 10 15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
 20 25 30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
 35 40 45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
 50 55 60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
 65 70 75 80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
 85 90 95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
 100 105 110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg

Sequence_Listing_R10901_Corrected.txt

```

115                               120       125
Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
130                               135       140

Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly
145                               150       155       160

Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His
165                               170       175

Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val
180                               185       190

Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly
195                               200       205

Arg Glx
210

```

```

<210> 96
<211> 461
<212> PRT
<213> Pseudomonas marcesans

```

```

<400> 96
Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn
 1      5      10      15

Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser
20      25      30

Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser
35      40      45

Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala
50      55      60

Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala
65      70      75      80

Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro
85      90      95

Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu
100     105     110

Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe
115     120     125

Asn Arg Phe Val Val Gly Pro Asn Ser Arg Met Ala His Ala Ala Ala
130     135     140

Met Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe Ile
145     150     155     160

Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile Gly
165     170     175

```

Sequence_Listing_R10901_Corrected.txt

```

His Tyr Arg Leu Glu Ile Asp Pro Gly Ala Lys Val Ser Tyr Val Ser
    180                      185                      190

Thr Glu Thr Phe Thr Asn Asp Leu Ile Leu Ala Ile Arg Gln Asp Arg
    195                      200                      205

Met Gln Ala Phe Arg Asp Arg Tyr Arg Ala Ala Asp Leu Ile Leu Val
    210                      215                      220

Asp Asp Ile Gln Phe Ile Glu Gly Lys Glu Tyr Thr Gln Glu Glu Phe
    225                      230                      235                      240

Phe His Thr Phe Asn Ala Leu His Asp Ala Gly Ser Gln Ile Val Leu
    245                      250                      255

Ala Ser Asp Arg Pro Pro Ser Gln Ile Pro Arg Leu Gln Glu Arg Leu
    260                      265                      270

Met Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Val Gln Ala Pro Asp
    275                      280                      285

Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu His Glu Arg
    290                      295                      300

Val Gly Leu Pro Arg Asp Leu Ile Gln Phe Ile Ala Gly Arg Phe Thr
    305                      310                      315                      320

Ser Asn Ile Arg Glu Leu Glu Gly Ala Leu Thr Arg Ala Ile Ala Phe
    325                      330                      335

Ala Ser Ile Thr Gly Leu Pro Met Thr Val Asp Ser Ile Ala Pro Met
    340                      345                      350

Leu Asp Pro Asn Gly Gln Gly Val Glu Val Thr Pro Lys Gln Val Leu
    355                      360                      365

Asp Lys Val Ala Glu Val Phe Lys Val Thr Pro Asp Glu Met Arg Ser
    370                      375                      380

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
    385                      390                      395                      400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr
    405                      410                      415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
    420                      425                      430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
    435                      440                      445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
    450                      455                      460

```

<210> 97
 <211> 447
 <212> PRT

Sequence_Listing_R10901_Corrected.txt

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
 1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
 20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
 35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
 50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
 65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
 85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
 100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
 115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
 130 135 140

Leu Cys Gly Gly Val Gly Leu Gly Lys Thr His Leu Met Gln Ala Ile
 145 150 155 160

Ala His Tyr Arg Leu Glu Met Tyr Pro Asn Ala Lys Val Tyr Tyr Val
 165 170 175

Ser Thr Glu Arg Phe Thr Asn Asp Leu Ile Thr Ala Ile Arg Gln Asp
 180 185 190

Asn Met Glu Asp Phe Arg Ser Tyr Tyr Arg Ser Ala Asp Phe Leu Leu
 195 200 205

Ile Asp Asp Ile Gln Phe Ile Lys Gly Lys Glu Tyr Thr Gln Glu Glu
 210 215 220

Phe Phe His Thr Phe Asn Ser Leu His Glu Ala Gly Lys Gln Val Val
 225 230 235 240

Val Ala Ser Asp Arg Ala Pro Gln Arg Ile Pro Gly Leu Gln Asp Arg
 245 250 255

Leu Ile Ser Arg Phe Ser Met Gly Leu Ile Ala Asp Ile Gln Val Pro
 260 265 270

Asp Leu Glu Thr Arg Met Ala Ile Leu Gln Lys Lys Ala Glu Tyr Asp
 275 280 285

Arg Ile Arg Leu Pro Lys Glu Val Ile Glu Tyr Ile Ala Ser His Tyr
 290 295 300

Sequence_Listing_R10901_Corrected.txt

Thr Ser Asn Ile Arg Glu Leu Gly Ala Leu Ile Arg Ala Ile Ala
305 310 315 320

Tyr Thr Ser Leu Ser Asn Val Ala Met Thr Val Glu Asn Ile Ala Pro
325 330 335

Val Leu Asn Pro Pro Val Glu Lys Val Ala Ala Ala Pro Glu Thr Ile
340 345 350

Ile Thr Ile Val Ala Gln His Tyr Gln Leu Lys Val Glu Glu Leu Leu
355 360 365

Ser Asn Ser Arg Arg Arg Glu Val Ser Leu Ala Arg Gln Val Gly Met
370 375 380

Tyr Leu Met Arg Gln His Thr Asp Leu Ser Leu Pro Arg Ile Gly Glu
385 390 395 400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Sequence_Listing_R10901_Corrected.txt

Ala	His	Ala	Ala	Ser	Leu	Ala	Val	Ala	Glu	Ala	Pro	Ala	Lys	Ala	Tyr	130	135	140
Asn	Pro	Leu	Phe	Ile	Tyr	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	145	150	155
Met	His	Ala	Ile	Gly	His	Tyr	Val	Ile	Asp	His	Asn	Pro	Ser	Ala	Lys	165	170	175
Val	Val	Tyr	Leu	Ser	Ser	Glu	Lys	Phe	Thr	Asn	Glu	Phe	Ile	Asn	Ser	180	185	190
Ile	Arg	Asp	Asn	Lys	Ala	Val	Asp	Phe	Arg	Asn	Arg	Tyr	Arg	Asn	Val	195	200	205
Asp	Val	Leu	Leu	Ile	Asp	Asp	Ile	Gln	Phe	Leu	Ala	Gly	Lys	Glu	Gln	210	215	220
Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn	Thr	Leu	His	Glu	Glu	Ser	225	230	235
Lys	Gln	Ile	Val	Ile	Ser	Ser	Asp	Arg	Pro	Pro	Lys	Glu	Ile	Pro	Thr	245	250	255
Leu	Glu	Asp	Arg	Leu	Arg	Ser	Arg	Phe	Glu	Trp	Gly	Leu	Ile	Thr	Asp	260	265	270
Ile	Thr	Pro	Pro	Asp	Leu	Glu	Thr	Arg	Ile	Ala	Ile	Leu	Arg	Lys	Lys	275	280	285
Ala	Lys	Ala	Glu	Gly	Leu	Asp	Ile	Pro	Asn	Glu	Val	Met	Leu	Tyr	Ile	290	295	300
Ala	Asn	Gln	Ile	Asp	Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	305	310	315
Arg	Val	Val	Ala	Tyr	Ser	Ser	Leu	Ile	Asn	Lys	Asp	Ile	Asn	Ala	Asp	325	330	335
Leu	Ala	Ala	Glu	Ala	Leu	Lys	Asp	Ile	Ile	Pro	Ser	Ser	Lys	Pro	Lys	340	345	350
Val	Ile	Thr	Ile	Lys	Glu	Ile	Gln	Arg	Val	Val	Gly	Gln	Gln	Phe	Asn	355	360	365
Ile	Lys	Leu	Glu	Asp	Phe	Lys	Ala	Lys	Lys	Arg	Thr	Lys	Ser	Val	Ala	370	375	380
Phe	Pro	Arg	Gln	Ile	Ala	Met	Tyr	Leu	Ser	Arg	Glu	Met	Thr	Asp	Ser	385	390	395
Ser	Leu	Pro	Lys	Ile	Gly	Glu	Glu	Phe	Gly	Gly	Arg	Asp	His	Thr	Thr	405	410	415
Val	Ile	His	Ala	His	Glu	Lys	Ile	Ser	Lys	Leu	Leu	Ala	Asp	Asp	Glu	420	425	430
Gln	Leu	Gln	Gln	His	Val	Lys	Glu	Ile	Lys	Glu	Gln	Leu	Lys			435	440	445

Sequence_Listing_R10901_Corrected.txt

<210> 99

<211> 507

<212> PRT

<213> Mycobacterium tuberculosis

<400> 99

```

Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1          5          10          15

Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
          20          25          30

Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
          35          40          45

Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
          50          55          60

Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
          65          70          75          80

Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
          85          90          95

Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
          100          105          110

Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
          115          120          125

Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
          130          135          140

His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
          145          150          155          160

Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
          165          170          175

Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
          180          185          190

Ile Ala Glu Ala Pro Ala Arg Ala Tyr Asn Pro Leu Phe Ile Trp Gly
          195          200          205

Glu Ser Gly Leu Gly Lys Thr His Leu Leu His Ala Ala Gly Asn Tyr
          210          215          220

Ala Gln Arg Leu Phe Pro Gly Met Arg Val Lys Tyr Val Ser Thr Glu
          225          230          235          240

Glu Phe Thr Asn Asp Phe Ile Asn Ser Leu Arg Asp Asp Arg Lys Val
          245          250          255

Ala Phe Lys Arg Ser Tyr Arg Asp Val Asp Val Leu Leu Val Asp Asp
          260          265          270

```

Sequence_Listing_R10901_Corrected.txt

```

Ile Gln Phe Ile Glu Gly Lys Glu Gly Ile Gln Glu Glu Phe Phe His
  275                                280                                285

Thr Phe Asn Thr Leu His Asn Ala Asn Lys Gln Ile Val Ile Ser Ser
  290                                295                                300

Asp Arg Pro Pro Lys Gln Leu Ala Thr Leu Glu Asp Arg Leu Arg Thr
  305                                310                                315                                320

Arg Phe Glu Trp Gly Leu Ile Thr Asp Val Gln Pro Pro Glu Leu Glu
  325                                330                                335

Thr Arg Ile Ala Ile Leu Arg Lys Lys Ala Gln Met Glu Arg Leu Ala
  340                                345                                350

Val Pro Asp Asp Val Leu Glu Leu Ile Ala Ser Ser Ile Glu Arg Asn
  355                                360                                365

Ile Arg Glu Leu Glu Gly Ala Leu Ile Arg Val Thr Ala Phe Ala Ser
  370                                375                                380

Leu Asn Lys Thr Pro Ile Asp Lys Ala Leu Ala Glu Ile Val Leu Arg
  385                                390                                395                                400

Asp Leu Ile Ala Asp Ala Asn Thr Met Gln Ile Ser Ala Ala Thr Ile
  405                                410                                415

Met Ala Ala Thr Ala Glu Tyr Phe Asp Thr Thr Val Glu Glu Leu Arg
  420                                425                                430

Gly Pro Gly Lys Thr Arg Ala Leu Ala Gln Ser Arg Gln Ile Ala Met
  435                                440                                445

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
  450                                455                                460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile
  465                                470                                475                                480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
  485                                490                                495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
  500                                505

```

<210> 100

<211> 446

<212> PRT

<213> Thermus thermophilus

<400> 100

```

Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
  1                                5                                10                                15

```

```

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
  20                                25                                30

```

```

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe

```

Sequence_Listing_R10901_Corrected.txt

```

35                               40 45
Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50                               55 60
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65                               70 75 80
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
                               85 90 95
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
          100          105 110
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
          115          120 125
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
          130          135 140
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
          145          150 155 160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
          165          170 175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
          180          185 190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe
          195          200 205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
          210          215 220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
          225          230 235 240
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
          245          250 255
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
          260          265 270
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
          275          280 285
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
          290          295 300
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
          305          310 315 320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
          325          330 335
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
          340          345 350

```

Sequence_Listing_R10901_Corrected.txt

Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
355 360 365

Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
370 375 380

Leu Thr Pro Ala Ser Leu Pro Glu Ile Gly Gln Leu Phe Gly Gly Arg
385 390 395 400

Asp His Thr Thr Val Arg Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala
405 410 415

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
1 5 10 15

Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Ala Arg Gln Val Ala Asp Asn
145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

Sequence_Listing_R10901_Corrected.txt

```

180                               185                               190
Lys Pro Asn Ala Lys Val Val Tyr Met His Ser Glu Arg Phe Val Gln
195                               200                               205
Asp Met Val Lys Ala Leu Gln Asn Asn Ala Ile Glu Glu Phe Lys Arg
210                               215                               220
Tyr Tyr Arg Ser Val Asp Ala Leu Leu Ile Asp Asp Ile Gln Phe Phe
225                               230                               235                               240
Ala Asn Lys Glu Arg Ser Gln Glu Glu Phe Phe His Thr Phe Asn Ala
245                               250                               255
Leu Leu Glu Gly Asn Gln Gln Ile Ile Leu Thr Ser Asp Arg Tyr Pro
260                               265                               270
Lys Glu Ile Asn Gly Val Glu Asp Arg Leu Lys Ser Arg Phe Gly Trp
275                               280                               285
Gly Leu Thr Val Ala Ile Glu Pro Pro Glu Leu Glu Thr Arg Val Ala
290                               295                               300
Ile Leu Met Lys Lys Ala Asp Glu Asn Asp Ile Arg Leu Pro Gly Glu
305                               310                               315                               320
Val Ala Phe Phe Ile Ala Lys Arg Leu Arg Ser Asn Val Arg Glu Leu
325                               330                               335
Glu Gly Ala Leu Asn Arg Val Ile Ala Asn Ala Asn Phe Thr Gly Arg
340                               345                               350
Ala Ile Thr Ile Asp Phe Val Arg Glu Ala Leu Arg Asp Leu Leu Ala
355                               360                               365
Leu Gln Glu Lys Leu Val Thr Ile Asp Asn Ile Gln Lys Thr Val Ala
370                               375                               380
Glu Tyr Tyr Lys Ile Lys Val Ala Asp Leu Leu Ser Lys Arg Arg Ser
385                               390                               395                               400
Arg Ser Val Ala Arg Pro Arg Gln Met Ala Met Ala Leu Ala Lys Glu
405                               410                               415
Leu Thr Asn His Ser Leu Pro Glu Ile Gly Asp Ala Phe Gly Gly Arg
420                               425                               430
Asp His Thr Thr Val Leu His Ala Cys Arg Lys Ile Glu Gln Leu Arg
435                               440                               445
Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
450                               455                               460
Leu Ser Ser
465

```

<210> 102

<211> 440

Sequence_Listing_R10901_Corrected.txt

<212> PRT

<213> *Thermatoga maritima*

<400> 102

Met	Lys	Glu	Arg	Ile	Leu	Gln	Glu	Ile	Lys	Thr	Arg	Val	Asn	Arg	Lys	1	5	10	15
Ser	Trp	Glu	Leu	Trp	Phe	Ser	Ser	Phe	Asp	Val	Lys	Ser	Ile	Glu	Gly	20	25	30	
Asn	Lys	Val	Val	Phe	Ser	Val	Gly	Asn	Leu	Phe	Ile	Lys	Glu	Trp	Leu	35	40	45	
Glu	Lys	Lys	Tyr	Tyr	Ser	Val	Leu	Ser	Lys	Ala	Val	Lys	Val	Val	Leu	50	55	60	
Gly	Asn	Asp	Ala	Thr	Phe	Glu	Ile	Thr	Tyr	Glu	Ala	Phe	Glu	Pro	His	65	70	75	80
Ser	Ser	Tyr	Ser	Glu	Pro	Leu	Val	Lys	Lys	Arg	Ala	Val	Leu	Leu	Thr	85	90	95	
Pro	Leu	Asn	Pro	Asp	Tyr	Thr	Phe	Glu	Asn	Phe	Val	Val	Gly	Pro	Gly	100	105	110	
Asn	Ser	Phe	Ala	Tyr	His	Ala	Ala	Leu	Glu	Val	Ala	Lys	His	Pro	Gly	115	120	125	
Arg	Tyr	Asn	Pro	Leu	Phe	Ile	Tyr	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	130	135	140	
His	Leu	Leu	Gln	Ser	Ile	Gly	Asn	Tyr	Val	Val	Gln	Asn	Glu	Pro	Asp	145	150	155	160
Leu	Arg	Val	Met	Tyr	Ile	Thr	Ser	Glu	Lys	Phe	Leu	Asn	Asp	Leu	Val	165	170	175	
Asp	Ser	Met	Lys	Glu	Gly	Lys	Leu	Asn	Glu	Phe	Arg	Glu	Lys	Tyr	Arg	180	185	190	
Lys	Lys	Val	Asp	Ile	Leu	Leu	Ile	Asp	Asp	Val	Gln	Phe	Leu	Ile	Gly	195	200	205	
Lys	Thr	Gly	Val	Gln	Thr	Glu	Leu	Phe	His	Thr	Phe	Asn	Glu	Leu	His	210	215	220	
Asp	Ser	Gly	Lys	Gln	Ile	Val	Ile	Cys	Ser	Asp	Arg	Glu	Pro	Gln	Lys	225	230	235	240
Leu	Ser	Glu	Phe	Gln	Asp	Arg	Leu	Val	Ser	Arg	Phe	Gln	Met	Gly	Leu	245	250	255	
Val	Ala	Lys	Leu	Glu	Pro	Pro	Asp	Glu	Glu	Thr	Arg	Lys	Ser	Ile	Ala	260	265	270	
Arg	Lys	Met	Leu	Glu	Ile	Glu	His	Gly	Glu	Leu	Pro	Glu	Glu	Val	Leu	275	280	285	
Asn	Phe	Val	Ala	Glu	Asn	Val	Asp	Asp	Asn	Leu	Arg	Arg	Leu	Arg	Gly				

Sequence_Listing_R10901_Corrected.txt

290

295

300

Ala Ile Ile Lys Leu Leu Val Tyr Lys Glu Thr Thr Gly Lys Glu Val
 305 310 315 320

Asp Leu Lys Glu Ala Ile Leu Leu Leu Lys Asp Phe Ile Lys Pro Asn
 325 330 335

Arg Val Lys Ala Met Asp Pro Ile Asp Glu Leu Ile Glu Ile Val Ala
 340 345 350

Lys Val Thr Gly Val Pro Arg Glu Glu Ile Leu Ser Asn Ser Arg Asn
 355 360 365

Val Lys Ala Leu Thr Ala Arg Arg Ile Gly Met Tyr Val Ala Lys Asn
 370 375 380

Tyr Leu Lys Ser Ser Leu Arg Thr Ile Ala Glu Lys Phe Asn Arg Ser
 385 390 395 400

His Pro Val Val Val Asp Ser Val Lys Lys Val Lys Asp Ser Leu Leu
 405 410 415

Lys Gly Asn Lys Gln Leu Lys Ala Leu Ile Asp Glu Val Ile Gly Glu
 420 425 430

Ile Ser Arg Arg Ala Leu Ser Gly
 435 440

<210> 103

<211> 457

<212> PRT

<213> Helicobacter pylori

<400> 103

Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
 1 5 10 15

Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
 20 25 30

Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
 35 40 45

Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
 50 55 60

Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
 65 70 75 80

His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
 85 90 95

Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
 100 105 110

Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
 115 120 125

Sequence_Listing_R10901_Corrected.txt

Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
 130 135 140
 Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
 145 150 155 160
 Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
 165 170 175
 Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
 180 185 190
 Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
 195 200 205
 Leu Leu Asp Asp Ala Gln Phe Leu Gln Gly Lys Pro Lys Leu Glu Glu
 210 215 220
 Glu Phe Phe His Thr Phe Asn Glu Leu His Ala Asn Ser Lys Gln Ile
 225 230 235 240
 Val Leu Ile Ser Asp Arg Ser Pro Lys Asn Ile Ala Gly Leu Glu Asp
 245 250 255
 Arg Leu Lys Ser Arg Phe Glu Trp Gly Ile Thr Ala Lys Val Met Pro
 260 265 270
 Pro Asp Leu Glu Thr Lys Leu Ser Ile Val Lys Gln Lys Cys Gln Leu
 275 280 285
 Asn Gln Ile Thr Leu Pro Glu Glu Val Met Glu Tyr Ile Ala Gln His
 290 295 300
 Ile Ser Asp Asn Ile Arg Gln Met Glu Gly Ala Ile Ile Lys Ile Ser
 305 310 315 320
 Val Asn Ala Asn Leu Met Asn Ala Ser Ile Asp Leu Asn Leu Ala Lys
 325 330 335
 Thr Val Leu Glu Asp Leu Gln Lys Asp His Ala Glu Gly Ser Ser Leu
 340 345 350
 Glu Asn Ile Leu Leu Ala Val Ala Gln Ser Leu Asn Leu Lys Ser Ser
 355 360 365
 Glu Ile Lys Val Ser Ser Arg Gln Lys Asn Val Ala Leu Ala Arg Lys
 370 375 380
 Leu Val Val Tyr Phe Ala Arg Leu Tyr Thr Pro Asn Pro Thr Leu Ser
 385 390 395 400
 Leu Ala Gln Phe Leu Asp Leu Lys Asp His Ser Ser Ile Ser Lys Met
 405 410 415
 Tyr Ser Gly Val Lys Lys Met Leu Glu Glu Lys Ser Pro Phe Val
 420 425 430
 Leu Ser Leu Arg Glu Glu Ile Lys Asn Arg Leu Asn Glu Leu Asn Asp

Sequence_Listing_R10901_Corrected.txt

435

440

445

Lys Lys Thr Ala Phe Asn Ser Ser Glu
450 455

<210> 104

<211> 1305

<212> DNA

<213> Thermus thermophilus

<400> 104

```

gtgtgcacag aggcgcgtctg gcaaacacgtt ctggagcaca tccgcgcag catcaccgag 60
gtggagttcc acacctgggtt tgaaaggatc cggcccttgg ggatccggga cggggtgctg 120
gagctcgccg tgcccacctc ctttgccctg gactggatcc ggcgccacta cggcggcctc 180
atccaggagg gccctcggtt cctcggggcc caggcgcccc ggtttgagct ccgggtggtg 240
cccggggtcg tagtcaggga ggacatcttc cagccccgc cgagcccccc ggcccaagct 300
caaccogaag atacctttaa aacttcgttg tggggcccaa caactccatg gcccacggc 360
ggcgccgtgg ccgtggccga gtccccggc cgggcctaca accccctctt catctacggg 420
ggccgtggcc tgggaaaagac ctacctgatg cagccgtgg gccactccg tgcgaagcgc 480
ttccccaca tgagattaga gtacgtttcc acggaaactt tcaccaacga gctcatcaac 540
cggccatccg cgagggaccg gatgacggag ttccgggagc ggtaccgctc cgtggacctc 600
ctgctggtgg acgacgtcca gtcatcgcc ggaaaggagc gcaccagga ggagttttc 660
cacaccttca acgcccctta cgaggccac aagcagatca tctctcctc cgaccggccg 720
cccaaggaca tctcaccct ggaggcgcgc ctgcggagcc gctttgagtg gggcctgatc 780
accgacaatc cagccccga cctggaaacc cggatcgcca tctgaagat gaacgccagc 840
agcgggcctg aggateccga ggacgcctg gactacatcg ccggcagggt cacctccaac 900
atccgggagt gggaaggggc cctcatgcgg gcacgcctt tgcctcctt caacggcgtt 960
gagctgaccc gcgcgtggc ggccaaggct ctccgacatc ttgcgccag ggagctggag 1020
gcggaccctt tggagatcat ccgcaaagcg gcgggaccag ttcggcctga aaccgccgga 1080
ggagctcacg gggagcgccg caagaaggag gtggtcctcc ccggcagct cgccatgtac 1140
ctggtgcggy agctcaccct ggccctcctg ccgagatcg accagctcaa cgacgaccgg 1200
gaccacacca cgtcctcta cgccatccag aaggtccagg agctcgcgga aagcgaccgg 1260
gaggtgcagg gctcctcctg caccctcgg gaggcgtgca catga 1305

```

<210> 105

<211> 434

<212> PRT

<213> Thermus thermophilus

<400> 105

```

Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1           5           10          15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20          25          30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35          40          45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50          55          60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65          70          75          80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85          90          95

```

Sequence_Listing_R10901_Corrected.txt

```

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
    100                      105                      110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
    115                      120                      125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
    130                      135                      140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
    145                      150                      155                      160

Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn
    165                      170                      175

Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg
    180                      185                      190

Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe
    195                      200                      205

Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn
    210                      215                      220

Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro
    225                      230                      235                      240

Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu
    245                      250                      255

Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile
    260                      265                      270

Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp
    275                      280                      285

Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp
    290                      295                      300

Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val
    305                      310                      315                      320

Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro
    325                      330                      335

Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly
    340                      345                      350

Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys
    355                      360                      365

Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu
    370                      375                      380

Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg
    385                      390                      395                      400

Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala

```

Sequence_Listing_R10901_Corrected.txt

405

410

415

Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala
 420 425 430

Cys Thr

<210> 106

<211> 1128

<212> DNA

<213> Thermus thermophilus

<400> 106

```

atgaacataa cggttcccaa aaaactcctc tcggaccagc tttccctcct ggagcgcac 60
gtccctctta gaagcgccaa cccctcttac acctacctgg ggctttacgc cgaggaagg 120
gcttgatcc tcttcgggac caacggggag gtggacctcg aggtccgcct ccccgccgag 180
gccccaaagc ttccccgggt gctcgcccc gccagccct tcttccagct ggtgcggagc 240
cttctgggg acctcggtggc cctcgccctc gcctcggagc cgggccaggg ggggcagctg 300
gagctctcct ccgggcgttt ccgcaccccg ctcagcctgg cccctgccga gggctacccc 360
gagcttctgg tgcccgaggg ggaggacaag ggggccttcc cctccggac gcggatgccc 420
tcgggggagc tcgtcaaggc cttgacccac gtgcgctacg ccgcgagcaa cgaggagtac 480
cgggccatct tcgcgggggt gcagctggag ttctccccc agggcttccg ggcggtggcc 540
tcgcacgggt accgcctcgc cctctacgac ctgcccctgc cccaagggtt ccaggccaag 600
gccgtggtcc ccgcccggag cgtggacgag atggtgcggg tctgaaggg ggcggacggg 660
gccgagggcg tctcgccct gggcgagggg gtgttggccc tggccctcga ggcggaagc 720
ggggtccgga tggccctccg cctcatggaa ggggagttcc ccgactacca gagggtcac 780
ccccaggagt tcgcccctcaa ggtccagggt gagggggagg ccctcaggga ggcggtgcgc 840
cgggtgagcg tctctcaga ccggcagaac caccgggtgg acctccttt ggaggaaggc 900
cggatcctcc tctccgcca gggggaactac ggcaagggc aggaggagg gcccgccag 960
gtggaggggc cggacatggc cgtggcctac aacgcccgt acctctcga ggcctcgc 1020
cccgtggggg accgggcca cctgggcac tcggggcca cgagcccag cctcatctg 1080
ggggacgggg aggggtaccg ggcggtggtg gtgcccctca ggtctag 1128

```

<210> 107

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 107

```

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
  1 5 10 15
Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
  20 25 30
Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
  35 40 45
Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
  50 55 60
Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
  65 70 75 80
Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
  85 90 95

```

Sequence_Listing_R10901_Corrected.txt

```

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
    100                      105                      110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
    115                      120                      125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
    130                      135                      140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
    145                      150                      155                      160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
    165                      170                      175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
    180                      185                      190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
    195                      200                      205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
    210                      215                      220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
    225                      230                      235                      240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
    245                      250                      255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
    260                      265                      270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
    275                      280                      285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
    290                      295                      300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
    305                      310                      315                      320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
    325                      330                      335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
    340                      345                      350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
    355                      360                      365

Val Val Val Pro Leu Arg Val Glx
    370                      375

```

<210> 108

<211> 376

<212> PRT

Sequence_Listing_R10901_Corrected.txt

<213> Thermus thermophilus

<400> 108

```

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1             5             10             15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
          20             25             30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35             40             45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50             55             60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65             70             75             80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
          85             90             95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
          100             105             110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
          115             120             125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
          130             135             140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
          145             150             155             160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
          165             170             175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
          180             185             190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
          195             200             205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
          210             215             220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
          225             230             235             240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
          245             250             255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
          260             265             270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
          275             280             285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
          290             295             300

```

Sequence_Listing_R10901_Corrected.txt

```

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
305                310                315                320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
                325                330                335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
                340                345                350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
                355                360                365

Val Val Val Pro Leu Arg Val Glx
370                375

```

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

```

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
 1                5                10                15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
                20                25                30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
                35                40                45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
 50                55                60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
65                70                75                80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
                85                90                95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
100                105                110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115                120                125

Thr Leu Pro Gln Ala Thr Met Lys Arg Leu Ile Glu Ala Thr Gln Phe
130                135                140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145                150                155                160

Glu Thr Glu Gly Glu Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
                165                170                175

Leu Ala Val Cys Ser Met Pro Ile Gly Gln Ser Leu Pro Ser His Ser
180                185                190

```

Sequence_Listing_R10901_Corrected.txt

```

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Met Leu Asp
  195                200                205

Gly Gly Asp Asn Pro Leu Arg Val Gln Ile Gly Ser Asn Asn Ile Arg
  210                215                220

Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly Arg
  225                230                235                240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Asp Lys His Leu
  245                250                255

Glu Ala Gly Cys Asp Leu Leu Lys Gln Ala Phe Ala Arg Ala Ala Ile
  260                265                270

Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Leu Tyr Val Ser Glu Asn
  275                280                285

Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu Glu
  290                295                300

Ile Leu Asp Val Thr Tyr Ser Gly Ala Glu Met Glu Ile Gly Phe Asn
  305                310                315                320

Val Ser Tyr Val Leu Asp Val Leu Asn Ala Leu Lys Cys Glu Asn Val
  325                330                335

Arg Met Met Leu Thr Asp Ser Val Ser Ser Val Gln Ile Glu Asp Ala
  340                345                350

Ala Ser Gln Ser Ala Ala Tyr Val Val Met Pro Met Arg Leu Glx
  355                360                365

```

<210> 110

<211> 367

<212> PRT

<213> Proteus mirabilis

<400> 110

```

Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln
  1                5                10                15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
  20                25                30

Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp
  35                40                45

Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu
  50                55                60

Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg
  65                70                75                80

Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg
  85                90                95

Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro

```

Sequence_Listing_R10901_Corrected.txt

```

100                               105                               110
Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe
115                               120                               125

Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe
130                               135                               140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe
145                               150                               155                               160

Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165                               170                               175

Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser
180                               185                               190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp
195                               200                               205

Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu
210                               215                               220

Arg Ala His Val Gly Asp Phe Ile Phe Thr Ser Lys Leu Val Asp Gly
225                               230                               235                               240

Arg Phe Pro Asp Tyr Arg Arg Val Leu Pro Lys Asn Pro Thr Lys Thr
245                               250                               255

Val Ile Ala Gly Cys Asp Ile Leu Lys Gln Ala Phe Ser Arg Ala Ala
260                               265                               270

Ile Leu Ser Asn Glu Lys Phe Arg Gly Val Arg Ile Asn Leu Thr Asn
275                               280                               285

Gly Gln Leu Lys Ile Thr Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
290                               295                               300

Glu Ile Val Asp Val Gln Tyr Gln Gly Glu Glu Met Glu Ile Gly Phe
305                               310                               315                               320

Asn Val Ser Tyr Leu Leu Asp Val Leu Asn Thr Leu Lys Cys Glu Glu
325                               330                               335

Val Lys Leu Leu Leu Thr Asp Ala Val Ser Ser Val Gln Val Glu Asn
340                               345                               350

Val Ala Ser Ala Ala Ala Ala Tyr Val Val Met Pro Met Arg Leu
355                               360                               365

```

<210> 111

<211> 366

<212> PRT

<213> Haemophilus influenzae

<400> 111

```

Met Gln Phe Ser Ile Ser Arg Glu Asn Leu Leu Lys Pro Leu Gln Gln
1           5           10           15

```


Sequence_Listing_R10901_Corrected.txt

```

Val Cys Gly Val Leu Ser Asn Arg Pro Asn Ile Pro Val Leu Asn Asn
    20                      25                      30

Val Leu Leu Gln Ile Glu Asp Tyr Arg Leu Thr Ile Thr Gly Thr Asp
    35                      40                      45

Leu Glu Val Glu Leu Ser Ser Gln Thr Gln Leu Ser Ser Ser Ser Glu
    50                      55                      60

Asn Gly Thr Phe Thr Ile Pro Ala Lys Lys Phe Leu Asp Ile Cys Arg
    65                      70                      75                      80

Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg
    85                      90                      95

Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro
   100                      105                      110

Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe
   115                      120                      125

Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe
   130                      135                      140

Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe
   145                      150                      155                      160

Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg
   165                      170                      175

Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser
   180                      185                      190

Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu
   195                      200                      205

Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg
   210                      215                      220

Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg
   225                      230                      235                      240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val
   245                      250                      255

Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile
   260                      265                      270

Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn
   275                      280                      285

Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu
   290                      295                      300

Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn
   305                      310                      315                      320

Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val

```

Sequence_Listing_R10901_Corrected.txt

325

330

335

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
 340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

<210> 112

<211> 367

<212> PRT

<213> Pseudomonas putida

<400> 112

Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
 1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His
 180 185 190

Gln Val Ile Val Pro Arg Lys Gly Ile Leu Glu Leu Ala Arg Leu Leu
 195 200 205

Thr Asp Pro Glu Gly Met Val Ser Ile Val Leu Gly Gln His His Ile
 210 215 220

Arg Ala Thr Thr Gly Glu Phe Thr Phe Thr Ser Lys Leu Val Asp Gly
 225 230 235 240

Sequence_Listing_R10901_Corrected.txt

Lys Phe Pro Asp Tyr Glu Arg Val Leu Pro Lys Gly Gly Asp Lys Leu
245 250 255

Val Val Gly Asp Arg Gln Ala Leu Arg Glu Ala Phe Ser Arg Thr Ala
260 265 270

Ile Leu Ser Asn Glu Lys Tyr Arg Gly Ile Arg Leu Gln Leu Ala Ala
275 280 285

Gly Gln Leu Lys Ile Gln Ala Asn Asn Pro Glu Gln Glu Glu Ala Glu
290 295 300

Glu Glu Ile Ser Val Asp Tyr Glu Gly Ser Ser Leu Glu Ile Gly Phe
305 310 315 320

Asn Val Ser Tyr Leu Leu Asp Val Leu Gly Val Met Thr Thr Glu Gln
325 330 335

Val Arg Leu Ile Leu Ser Asp Ser Asn Ser Ser Ala Leu Leu Gln Glu
340 345 350

Ala Gly Asn Asp Asp Ser Ser Tyr Val Val Met Pro Met Arg Leu
355 360 365

<210> 113

<211> 366

<212> PRT

<213> Buchnera aphidicola

<400> 113

Met Lys Phe Thr Ile Gln Asn Asp Ile Leu Thr Lys Asn Leu Lys Lys
1 5 10 15

Ile Thr Arg Val Leu Val Lys Asn Ile Ser Phe Pro Ile Leu Glu Asn
20 25 30

Ile Leu Ile Gln Val Glu Asp Gly Thr Leu Ser Leu Thr Thr Thr Asn
35 40 45

Leu Glu Ile Glu Leu Ile Ser Lys Ile Glu Ile Ile Thr Lys Tyr Ile
50 55 60

Pro Gly Lys Thr Thr Ile Ser Gly Arg Lys Ile Leu Asn Ile Cys Arg
65 70 75 80

Thr Leu Ser Glu Lys Ser Lys Ile Lys Met Gln Leu Lys Asn Lys Lys
85 90 95

Met Tyr Ile Ser Ser Glu Asn Ser Asn Tyr Ile Leu Ser Thr Leu Ser
100 105 110

Ala Asp Thr Phe Pro Asn His Gln Asn Phe Asp Tyr Ile Ser Lys Phe
115 120 125

Asp Ile Ser Ser Asn Ile Leu Lys Glu Met Ile Glu Lys Thr Glu Phe
130 135 140

Sequence_Listing_R10901_Corrected.txt

```

Ser Met Gly Lys Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
145                      150                      155                      160

Glu Lys Lys Asp Lys Phe Leu Arg Ser Val Ala Thr Asp Gly Tyr Arg
                      165                      170                      175

Leu Ala Ile Ser Tyr Thr Gln Leu Lys Lys Asp Ile Asn Phe Phe Ser
                      180                      185                      190

Ile Ile Ile Pro Asn Lys Ala Val Met Glu Leu Leu Lys Leu Leu Asn
                      195                      200                      205

Thr Gln Pro Gln Leu Leu Asn Ile Leu Ile Gly Ser Asn Ser Ile Arg
                      210                      215                      220

Ile Tyr Thr Lys Asn Leu Ile Phe Thr Thr Gln Leu Ile Glu Gly Glu
225                      230                      235                      240

Tyr Pro Asp Tyr Lys Ser Val Leu Phe Lys Glu Lys Lys Asn Pro Ile
                      245                      250                      255

Ile Thr Asn Ser Ile Leu Leu Lys Lys Ser Leu Leu Arg Val Ala Ile
                      260                      265                      270

Leu Ala His Glu Lys Phe Cys Gly Ile Glu Ile Lys Ile Glu Asn Gly
                      275                      280                      285

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
                      290                      295                      300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
305                      310                      315                      320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
                      325                      330                      335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
                      340                      345                      350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
                      355                      360                      365

```

<210> 114

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 114

gtgtggatcc tcgtcccccct catgcgcgac caggaaggg

39

<210> 115

<211> 27

<212> DNA

<213> Artificial Sequence

Sequence_Listing_R10901_Corrected.txt

<220>

<223> Description of Artificial Sequence: primer

<400> 115

gtgtggatcc gtggtgacct tagccac

27

<210> 116

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 116

ttcgtgtccg aggaccttgt ggtccacaac

30

<210> 117

<211> 3514

<212> DNA

<213> Aquifex aeolicus

<400> 117

```

atgagtaagg atttcgtcca ccttcacctg cacacccagt tctcactcct ggacggggct 60
ataaagatag acgagctcgt gaaaaaaggca aaggagtatg gatacaaaagc tgtcgggaatg 120
tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaagga 180
attaagccca taatcggcat ggaagcctac tttaccacgg gttcgaggtt tgacagaaaag 240
actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
aaggacgaaa aggtctaaaag aacttaatga agctctcaac cctcgccctac aaagaagggt 360
tttactacaa acccagaatt gattacgaac tccttgaaaa gtacggggag ggctaataag 420
cccttaccgc atgcctgaaa ggtgttccca cctactacgc ttctataaac gaagtgaaaa 480
aggcggagga atgggtaaaag aagttcaagg atatattcgg agatgacctt tatttagaac 540
ttcaagcgaa caacattcca gaacaggaag tggcaaacag gaacttaata gagatagcca 600
aaaagtacga tgtgaaactc atagcgacgc aggaagccca ctacctcaat ccggaagaca 660
ggtacgcccc cacggttctt atggcacttc aaatgaaaaa gaccattcac gaactgagtt 720
cgggaaactt caagtgttca aacgaagacc ttcactttgc tccacccgag tacatgtgga 780
aaaagtttga aggttaagttc gaaggctggg aaaaggcact cctgaacact ctcgaggtaa 840
tggaagagac agcggacagc tttgagatat ttgaaaactc cacctacctc cttcccaagt 900
acgacgttcc gcccgacaaa acccttgagg aatacctcag agaactcgcg taaaaaggtt 960
taagacagag gatagaaagg ggacaagcta aggatactaa agagtactgg gagaggctcg 1020
agtacgaact ggaagtata aacaaaatgg gctttgcggg atacttcttg atagttcagg 1080
acttcataaa ctgggctaag aaaaacgaca tacctgttgg acccggaagg ggaagtgcctg 1140
gaggttccct cgtcgcatat gccatcggaa taacggacgt tgacctata aagcacggat 1200
tcctttttga gaggttctta aaccccgaaa gggtttccat gccggatata gacgtggatt 1260
tctgtcagga caacagggaa aaggtcatag agtacgtaag gaacaagtac ggacacgaca 1320
acgtagctca gataatcacc tacaacgtaa tgaaggcgaa gcaaaactg agagacgtcg 1380
caagggccat gggactcccc tactccaccg cggacaaaact cgaaaactc attcctcagg 1440
gggacgttca ggaacgttg ctcagtcctg aagagatgta caaaacgcct gtggaggaac 1500
tccttcagaa gtacggagaa cacagaacgg acatagagga caacgtaaaag aagttcagac 1560
agatatgcga agaaagtccg gagataaaac agctcgttga gacggccctg aagcttgaag 1620
gtctcacgag acacacctcc ctccacgcgg cgggagtggg tatagacca aagcccttga 1680
gogagctcgt tcccctctac tacgataaag agggcgaagt cgcaaccag tacgacatgg 1740
ttcagctcga agaactcggg ctccctgaaga tggacttccg cggactcaaa accctcacag 1800
aactgaaact catgaaagaa ctcataaagg aaagacacgg agtggatata aacttccctg 1860
aacttccctc tgacgacccg aaagtgttaca aactccttca ggaaggaaaa accacgggag 1920
tgttccagct cgaaagcagg ggaatgaaag aactcctgaa gaaactaaag cccgacagct 1980

```

Sequence_Listing_R10901_Corrected.txt

```

ttgacgacat cgttgcggtc ctgcactct acagaccgg accctctaaag agcggactcg 2040
ttgacacata cattaagaga aagcacggaa aagaaccggt tgagtacccc ttcccggagc 2100
ttgaaccggt ccttaaggaa acctacggag taatcgttta tcaggaacag gtgatgaaga 2160
tgtctcagat actttccggc tttactcccg gagaggcgga taccctcaga aaggcgatag 2220
gtaagaagaa agcggattta atggctcaga tgaaagacaa gttcatacag ggagcgggtg 2280
aaaggggata ccctgaagaa aagataagga agctctggga agacatagag aagtctgctt 2340
cctactcctt caacaagtct cactcggtag cttacgggta catctcctac tggaccgcct 2400
acgttaaagc ccactatccc gcggagttct tcgcggtaaa actcacaact gaaaagaacg 2460
acaacaagtt cctcaacctc ataaaagaag ctaaactctt cggatttgag atacttcccc 2520
ccgacataaa caagagtgat gtaggattta cgatagaagg tgaaaacagg ataagggttcg 2580
ggcttgcgag gataaaggga gtgggagagg aaactgctaa gataatcggt gaagctagaa 2640
agaagtataa gcagttcaaa gggcttgogg acttcataaa caaaaccaag aacaggaaga 2700
taaacaagaa agtcgtggaa gcaactgtaa aggcaggggc ttttgacttt actaagaaaa 2760
agaggaaaga actactcgct aaagtggcaa actctgaaaa agcattaatg gctacacaaa 2820
actccctttt cgggtgcaccg aaagaagaag tggaagaact cgaccocctt aagcttgaaa 2880
aggaagttct cggttttttac atttcagggc acccccttga caactacgaa aagctcctca 2940
agaaccgcta cacaccocatt gaagatttag aagagtggga caaggaaagc gaagcgggtc 3000
ttacaggagt tatcacggaa ctcaaagtaa aaaagacgaa aaacggagat tacatggcgg 3060
tcttcaacct cgttgacaag acgggactaa tagagtgtgt cgtcttcccg ggagtttaacg 3120
aagaggcaaa ggaactgata gaagaggaca gagtagtgt agtcaaaggt tttctggaacg 3180
aggacottga aacggaaaat gtcaagttcg tggtgaaaga ggttttctcc cctgaggagt 3240
tcgcaaagga gatgaggaat accotttata tattottaaa aagagagcaa gccctaaacg 3300
gcgttgccga aaaactaaag ggaattattg aaaacaacag gacggaggac ggatacaact 3360
tggtttctcag ggttgatctg ggagactact tcgttgattt agcactccca caagatatga 3420
aactaaaggc tgacagaaag gttgtagagg agatagaaaa actgggagtg aagggtcataa 3480
tttagtaaat aacccttact tccgagtagt cccc 3514

```

<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

```

Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
 1             5             10             15

```

```

Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
      20             25             30

```

```

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
    35             40             45

```

```

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
    50             55             60

```

```

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
    65             70             75             80

```

```

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
      85             90             95

```

```

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu
    100            105            110

```

```

Ser Thr Leu Ala Tyr Lys Glu Gly Phe Tyr Tyr Lys Pro Arg Ile Asp
    115            120            125

```

```

Tyr Glu Leu Leu Glu Lys Tyr Gly Glu Gly Leu Ile Ala Leu Thr Ala

```

130

140

Cys 145	Leu	Lys	Gly	Val	Pro 150	Thr	Tyr	Tyr	Ala	Ser 155	Ile	Asn	Glu	Val	Lys 160
Lys	Ala	Glu	Glu	Trp 165	Val	Lys	Lys	Phe	Lys 170	Asp	Ile	Phe	Gly	Asp 175	Asp
Leu	Tyr	Leu	Glu 180	Leu	Gln	Ala	Asn 185	Asn	Ile	Pro	Glu	Gln	Glu	Val	Ala
Asn	Arg	Asn 195	Leu	Ile	Glu	Ile	Ala 200	Lys	Lys	Tyr	Asp	Val 205	Lys	Leu	Ile
Ala	Thr 210	Gln	Asp	Ala	His	Tyr 215	Leu	Asn	Pro	Glu	Asp 220	Arg	Tyr	Ala	His
Thr 225	Val	Leu	Met	Ala 230	Leu	Gln	Met	Lys	Lys	Thr 235	Ile	His	Glu	Leu	Ser 240
Ser	Gly	Asn	Phe	Lys 245	Cys	Ser	Asn	Glu	Asp 250	Leu	His	Phe	Ala	Pro 255	Pro
Glu	Tyr	Met	Trp 260	Lys	Lys	Phe	Glu	Gly 265	Lys	Phe	Glu	Gly	Trp 270	Glu	Lys
Ala	Leu 275	Leu	Asn	Thr	Leu	Glu	Val 280	Met	Glu	Lys	Thr	Ala 285	Asp	Ser	Phe
Glu	Ile 290	Phe	Glu	Asn	Ser	Thr 295	Tyr	Leu	Leu	Pro	Lys 300	Tyr	Asp	Val	Pro
Pro 305	Asp	Lys	Thr	Leu 310	Glu	Glu	Tyr	Leu	Arg	Glu 315	Leu	Ala	Tyr	Lys	Gly 320
Leu	Arg	Gln	Arg	Ile 325	Glu	Arg	Gly	Gln	Ala 330	Lys	Asp	Thr	Lys	Glu 335	Tyr
Trp	Glu	Arg	Leu 340	Glu	Tyr	Glu	Leu	Glu 345	Val	Ile	Asn	Lys	Met 350	Gly	Phe
Ala	Gly 355	Tyr	Phe	Leu	Ile	Val	Gln 360	Asp	Phe	Ile	Asn	Trp 365	Ala	Lys	Lys
Asn	Asp 370	Ile	Pro	Val	Gly	Pro 375	Gly	Arg	Gly	Ser	Ala 380	Gly	Gly	Ser	Leu
Val 385	Ala	Tyr	Ala	Ile 390	Gly	Ile	Thr	Asp	Val	Asp 395	Pro	Ile	Lys	His	Gly 400
Phe	Leu	Phe	Glu	Arg 405	Phe	Leu	Asn	Pro	Glu 410	Arg	Val	Ser	Met	Pro 415	Asp
Ile	Asp	Val	Asp 420	Phe	Cys	Gln	Asp	Asn 425	Arg	Glu	Lys	Val	Ile 430	Glu	Tyr
Val	Arg 435	Asn	Lys	Tyr	Gly	His 440	Asp	Asn	Val	Ala	Gln 445	Ile	Ile	Thr	Tyr

Sequence Listing_R10901_Corrected.txt

```

Asn Val Met Lys Ala Lys Gln Thr Leu Arg Asp Val Ala Arg Ala Met
450                               455                               460

Gly Leu Pro Tyr Ser Thr Ala Asp Lys Leu Ala Lys Leu Ile Pro Gln
465                               470                               475                               480

Gly Asp Val Gln Gly Thr Trp Leu Ser Leu Glu Glu Met Tyr Lys Thr
                               485                               490                               495

Pro Val Glu Glu Leu Leu Gln Lys Tyr Gly Glu His Arg Thr Asp Ile
                               500                               505                               510

Glu Asp Asn Val Lys Lys Phe Arg Gln Ile Cys Glu Glu Ser Pro Glu
515                               520                               525

Ile Lys Gln Leu Val Glu Thr Ala Leu Lys Leu Glu Gly Leu Thr Arg
530                               535                               540

His Thr Ser Leu His Ala Ala Gly Val Val Ile Ala Pro Lys Pro Leu
545                               550                               555                               560

Ser Glu Leu Val Pro Leu Tyr Tyr Asp Lys Glu Gly Glu Val Ala Thr
                               565                               570                               575

Gln Tyr Asp Met Val Gln Leu Glu Glu Leu Gly Leu Leu Lys Met Asp
580                               585                               590

Phe Leu Gly Leu Lys Thr Leu Thr Glu Leu Lys Leu Met Lys Glu Leu
595                               600                               605

Ile Lys Glu Arg His Gly Val Asp Ile Asn Phe Leu Glu Leu Pro Leu
610                               615                               620

Asp Asp Pro Lys Val Tyr Lys Leu Leu Gln Glu Gly Lys Thr Thr Gly
625                               630                               635                               640

Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu Leu Leu Lys Lys Leu
645                               650                               655

Lys Pro Asp Ser Phe Asp Asp Ile Val Ala Val Leu Ala Leu Tyr Arg
660                               665                               670

Pro Gly Pro Leu Lys Ser Gly Leu Val Asp Thr Tyr Ile Lys Arg Lys
675                               680                               685

His Gly Lys Glu Pro Val Glu Tyr Pro Phe Pro Glu Leu Glu Pro Val
690                               695                               700

Leu Lys Glu Thr Tyr Gly Val Ile Val Tyr Gln Glu Gln Val Met Lys
705                               710                               715                               720

Met Ser Gln Ile Leu Ser Gly Phe Thr Pro Gly Glu Ala Asp Thr Leu
725                               730                               735

Arg Lys Ala Ile Gly Lys Lys Lys Ala Asp Leu Met Ala Gln Met Lys
740                               745                               750

Asp Lys Phe Ile Gln Gly Ala Val Glu Arg Gly Tyr Pro Glu Glu Lys
755                               760                               765

```


Sequence_Listing_R10901_Corrected.txt

```

Ile Arg Lys Leu Trp Glu Asp Ile Glu Lys Phe Ala Ser Tyr Ser Phe
770                      775                      780

Asn Lys Ser His Ser Val Ala Tyr Gly Tyr Ile Ser Tyr Trp Thr Ala
785                      790                      795                      800

Tyr Val Lys Ala His Tyr Pro Ala Glu Phe Phe Ala Val Lys Leu Thr
                        805                      810                      815

Thr Glu Lys Asn Asp Asn Lys Phe Leu Asn Leu Ile Lys Asp Ala Lys
                        820                      825                      830

Leu Phe Gly Phe Glu Ile Leu Pro Pro Asp Ile Asn Lys Ser Asp Val
835                      840                      845

Gly Phe Thr Ile Glu Gly Glu Asn Arg Ile Arg Phe Gly Leu Ala Arg
850                      855                      860

Ile Lys Gly Val Gly Glu Glu Thr Ala Lys Ile Ile Val Glu Ala Arg
865                      870                      875                      880

Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr
                        885                      890                      895

Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala
900                      905                      910

Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys
915                      920                      925

Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe
930                      935                      940

Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu
945                      950                      955                      960

Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr
965                      970                      975

Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu
980                      985                      990

Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu
995                      1000                      1005

Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu
1010                      1015                      1020

Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr
1025                      1030                      1035                      1040

Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys
1045                      1050                      1055

Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val
1060                      1065                      1070

Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr

```

Sequence_Listing_R10901_Corrected.txt

1075

1080

1085

Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu
 1090 1095 1100

Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn
 1105 1110 1115 1120

Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu
 1125 1130 1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
 1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
 1155 1160

<210> 119

<211> 2408

<212> DNA

<213> Aquifex aeolicus

<400> 119

atgaactacg ttcccttgcg gagaaagtac agaccgaaat tcttcagggg agtaaatagga 60
 caggaagctc ccgtaaggat actcaaaaac gctataaaaa acgacagagt ggctcacgcc 120
 tacctctttg ccggaccgag ggggggttggg aagacgacta ttgcaagaat tctcgcaaaa 180
 gctttgaact gtaaaaatcc ctccaaagggt gagccctgcg gtgagtgcga aaactgcagg 240
 gagatagaca ggggtgtgtt cctcgactta attgaaatgg atgcgcctc aaacaggggt 300
 atagacgacg taagggcatt aaaagaagcg gtcaattaca aacctataaa aggaaagtac 360
 aaggtttaca taatagacga agctcacatg ctacagaaag aagctttcaa cgctctctta 420
 aaaaccctcg aagagccccc tccagaact gtttctgccc tttgtaccac ggagtacgac 480
 aaaattcttc ccacgatact ctcaagggtgt cagaggataa tcttctcaaa ggtaagaaa 540
 gaaaaagtaa tagagtatct aaaaaagata tgtgaaaagg aagggattga gtgcgaagag 600
 ggagcccttg aggttctggc tcatgcctct gaagggtgca tgagggatgc agcctctctc 660
 ctggaccagg cgagcgttta cggggaaggc agggtaacaa aagaagtagt ggagaacttc 720
 ctcggaattc tcagtcagga aagcgttagg agttttctga aattgcttct gaactcagaa 780
 gtggacgaag ctataaagtt cctcagagaa ctctcagaaa agggctacaa cctgaccaag 840
 ttttgggaga tggttagaaga ggaagtgaga aacgcaattt tagtaaagag cctgaaaaat 900
 cccgaaagcg tggttcagaa ctggcaggat tacgaagact tcaaagacta cctctggaa 960
 gccctcctct acgttgagaa cctgataaac aggggtaaaag ttgaagcgag aacgagagaa 1020
 cccttaagag cctttgaact cgcggttaata aagagcctta tagtcaaaga cataattccc 1080
 gtatcccagc tcggaagtgt ggtaaaggaa accaaaaagg aagaaaagaa agttgaagta 1140
 aaagaagagc caaaagttaa agaagaaaaa ccaaaggagc aggaagagga caggttccag 1200
 aaagtthtaa acgctgtgga cggcaaaatc cttaaaagaa tacttgaagg ggcaaaaagg 1260
 gaagaaagag acggaaaaaat cgtcctaaag atagaagcct cttatctgag aacctgaaa 1320
 aaggaatttg actcactaaa ggagactttt ccttttttag agtttgaacc cgtggaggat 1380
 aaaaaaaaac ctccagaagtc cagcgggacg aggcgtgttt aaaggtaaag gagctcttca 1440
 atgcaaaaat actcaaagta cgaagtaaaa gctaagggtc taaagggtgag aatgcccgtg 1500
 gaagagatag ggctgtttta cgcactaata gacggcttgc ccaggtagcg actcacgagg 1560
 acgaaggaaa agggaaagggt agaagttttc gtttttagcg ctctttataa agtcaaggaa 1620
 ttgatggaag ctatggaggg tatgaaaaaa cacataaagg atttagaaat cctcgagag 1680
 acggatgagg atttaacttt ttaaagtatg ggtgtatctg agcaaagggt taagctaaaa 1740
 acaaacctga aacccgcagg ggaccagccg aaagccataa aaaaactcct tgaaaacct 1800
 aggaaaggcg taaaagaaca aacacttctc ggagtcacgg gaagcggaaa gacttttact 1860
 ctagcaaacg taatagcgaa gtacaacaaa ccaactcttg tggtagtcca caacaaaatt 1920
 ctgcgggcac agctatacag ggagttttaa gaactattcc ctgaaaacgc tgtagagtac 1980
 tttgtctctt actacgacta ttaccaacct gaagcctaca ttcccgaaaa agattttatac 2040
 atagaaaagg acgcgagtat aaacgaaagc tggaacggtt cagacactcc gccacgatat 2100

Sequence_Listing_R10901_Corrected.txt

```

ccgttctaga aaggagggac gttatagtag ttgtttcagt ttcttgcata tacggactcg 2160
ggaaacctga gcactacgaa aacctgagga taaaactcca aaggggaata agactgaact 2220
tgagtaagct cctgaggaaa ctogttgagc taggatatca gagaaatgac ttgccataa 2280
agagggctac cttctcggtt aggggagacg tggttgagat agtcccttct cacacggaag 2340
attacctcgt gagggtagag ttctgggacg acgaagtga aagaatagtc ctcatggacg 2400
ctctgaac 2408

```

<210> 120

<211> 473

<212> PRT

<213> Aquifex aeolicus

<400> 120

```

Met Asn Tyr Val Pro Phe Ala Arg Lys Tyr Arg Pro Lys Phe Phe Arg
  1             5             10             15

```

```

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
      20             25             30

```

```

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
      35             40             45

```

```

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
      50             55             60

```

```

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
      65             70             75             80

```

```

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
      85             90             95

```

```

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
     100             105             110

```

```

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
     115             120             125

```

```

His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
     130             135             140

```

```

Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
     145             150             155             160

```

```

Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
     165             170             175

```

```

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
     180             185             190

```

```

Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
     195             200             205

```

```

Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
     210             215             220

```

```

Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
     225             230             235             240

```

Sequence_Listing_R10901_Corrected.txt

```

Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
    245                      250                      255

Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
    260                      265                      270

Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
    275                      280                      285

Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
    290                      295                      300

Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
    305                      310                      315                      320

Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
    325                      330                      335

Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
    340                      345                      350

Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
    355                      360                      365

Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
    370                      375                      380

Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
    385                      390                      395                      400

Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
    405                      410                      415

Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
    420                      425                      430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
    435                      440                      445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
    450                      455                      460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
    465                      470

```

<210> 121

<211> 1090

<212> DNA

<213> Aquifex aeolicus

<400> 121

```

atgcgcgttta aggtggacag ggaggagctt gaagaggttc ttaaaaaagc aagagaaagc 60
acggaaaaaaa aagccgcact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120
aacttaatcg taagggcaac ggacttggaa aactaccttg tagtctccgt aaagggggag 180
gttgaagagg aaggagaggt ttgcgtccac tctcaaaaac tctacgatat agtcaagaac 240
ttaaatccg cttacgttta ctttcatacg gaaggtgaaa aactcgtcat aacggggagga 300
aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
gtagaaggag gagaaacact ttcgggaaac cttctcgtta acggaataga aaaggtagag 420

```

Sequence_Listing_R10901_Corrected.txt

```

tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480
gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540
taaacattga aaagagtgaag gacgagtctt ttgcttactt ctccactccc gagtggaaac 600
tcgcgcgttag ctccctggaag gagaattccc ggactacatg agtgtcatcc ctgaggagtt 660
ttcgcgcggaa gtcttggttg agacagagga agtcttaaag gttttaaaaga ggttgaaggc 720
tttaagcgaa ggaaaagtgt ttcccgtaga gattacctta agcgaaaacc ttgccatctt 780
tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840
agagcccttt gagataggat tcaacggaaa tacottatgg aggcgcttga cgcctacgac 900
agcgaaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960
gattacgaaa aggaacctta caagtgcata ataatgcga tgagggtgta gccatgaaaa 1020
aagctttaat ctttttattg agcttgagcc ttttaattcc tgcgttttagc gaagccaaac 1080
ccaagtcttc                                     1090

```

<210> 122

<211> 363

<212> PRT

<213> Aquifex aeolicus

<400> 122

```

Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys
  1              5              10              15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn
          20              25              30

Phe Leu Leu Ser Ala Lys Glu Glu Asn Leu Ile Val Arg Ala Thr Asp
          35              40              45

Leu Glu Asn Tyr Leu Val Val Ser Val Lys Gly Glu Val Glu Glu Glu
          50              55              60

Gly Glu Val Cys Val His Ser Gln Lys Leu Tyr Asp Ile Val Lys Asn
          65              70              75              80

Leu Asn Ser Ala Tyr Val Tyr Leu His Thr Glu Gly Glu Lys Leu Val
          85              90              95

Ile Thr Gly Gly Lys Ser Thr Tyr Lys Leu Pro Thr Ala Pro Ala Glu
          100             105             110

Asp Phe Pro Glu Phe Pro Glu Ile Val Glu Gly Gly Glu Thr Leu Ser
          115             120             125

Gly Asn Leu Leu Val Asn Gly Ile Glu Lys Val Glu Tyr Ala Ile Ala
          130             135             140

Lys Glu Glu Ala Asn Ile Ala Leu Gln Gly Met Tyr Leu Arg Gly Tyr
          145             150             155             160

Glu Asp Arg Ile His Phe Val Gly Ser Asp Gly His Arg Leu Ala Leu
          165             170             175

Tyr Glu Pro Leu Gly Glu Phe Ser Lys Glu Leu Leu Ile Pro Arg Lys
          180             185             190

Ser Leu Lys Val Leu Lys Lys Leu Ile Thr Gly Ile Glu Asp Val Asn
          195             200             205

```

Sequence_Listing_R10901_Corrected.txt

```

Ile Glu Lys Ser Glu Asp Glu Ser Phe Ala Tyr Phe Ser Thr Pro Glu
 210                215                220

Trp Lys Leu Ala Val Arg Leu Leu Glu Gly Glu Phe Pro Asp Tyr Met
225                230                235                240

Ser Val Ile Pro Glu Glu Phe Ser Ala Glu Val Leu Phe Glu Thr Glu
                245                250                255

Glu Val Leu Lys Val Leu Lys Arg Leu Lys Ala Leu Ser Glu Gly Lys
                260                265                270

Val Phe Pro Val Lys Ile Thr Leu Ser Glu Asn Leu Ala Ile Phe Glu
                275                280                285

Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu
                290                295                300

Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met
305                310                315                320

Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr
                325                330                335

Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu
                340                345                350

Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val
    355                360

```

<210> 123

<211> 1093

<212> DNA

<213> Aquifex aeolicus

<400> 123

```

gtggaaacca caatatcca gttccagaaa acttttttca caaaacctcc gaaggagagg 60
gtcttcgtcc ttcattggaga agagcagtat ctcataagaa cctttttgtc taagctgaag 120
gaaaagtacg gggagaatta cacggttctg tgggggggatg agataagcga ggagggaattc 180
tacactgccc ttcccgagac cagtatatc ggcggttcaa aggaaaaagc ggtggtcatt 240
tacaacttgc gggatttcct gaagaagctc ggaaggaaga aaaaggaaaa agaaaggctt 300
ataaaaagtc tcagaaaacgt aaagagtaac tacgtattta tagtgtacga tgcgaaactc 360
cagaaaacagg aactttcttc ggaacctctg aaatccgtag cgtctttcgg cggtatagt 420
gtagcaaaaca ggctgagcaa ggagaggata aaacagctcg tccttaagaa gttcaaagaa 480
aaagggataa acgtagaaaa cgatgccctt gaataccttc tcagctcac gggttacaac 540
ttgatggagc tcaaacttga ggttgaaaaa ctgatagatt acgcaagtga aaagaaaatt 600
ttaacactcg atgaggtaaa gagagtagcc ttctcagctc cagaaaacgt aaacgtattt 660
gagttcgttg atttactcct cttaaaaagat tacgaaaagg ctcttaaaagt tttggactcc 720
ctcatttcct tcggaatata ccccttcag attatgaaaa tcctgtcctc ctatgctcta 780
aaactttaca cctcaagag gcttgaagag aaggagagg acctgaataa ggcgatggaa 840
agcgtgggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900
tctaaagagg acttgaagaa cctaactctc tccctccaga ggatagacgc tttttctaaa 960
ctttactttc aggacacagt gcagttgctg gggatttctt gacctcaaga ctggagaggg 1020
aagttgtgaa aaatacttct catggtggat aatctttttt atgaagtttg cggtttgcgt 1080
ttttccgggt tct                                     1093

```

<210> 124

Sequence_Listing_R10901_Corrected.txt

<211> 350

<212> PRT

<213> Aquifex aeolicus

<400> 124

```

Val Glu Thr Thr Ile Phe Gln Phe Gln Lys Thr Phe Phe Thr Lys Pro
  1              5              10              15

Pro Lys Glu Arg Val Phe Val Leu His Gly Glu Glu Gln Tyr Leu Ile
      20              25              30

Arg Thr Phe Leu Ser Lys Leu Lys Glu Lys Tyr Gly Glu Asn Tyr Thr
      35              40              45

Val Leu Trp Gly Asp Glu Ile Ser Glu Glu Glu Phe Tyr Thr Ala Leu
      50              55              60

Ser Glu Thr Ser Ile Phe Gly Gly Ser Lys Glu Lys Ala Val Val Ile
      65              70              75              80

Tyr Asn Phe Gly Asp Phe Leu Lys Lys Leu Gly Arg Lys Lys Lys Glu
      85              90              95

Lys Glu Arg Leu Ile Lys Val Leu Arg Asn Val Lys Ser Asn Tyr Val
      100              105              110

Phe Ile Val Tyr Asp Ala Lys Leu Gln Lys Gln Glu Leu Ser Ser Glu
      115              120              125

Pro Leu Lys Ser Val Ala Ser Phe Gly Gly Ile Val Val Ala Asn Arg
      130              135              140

Leu Ser Lys Glu Arg Ile Lys Gln Leu Val Leu Lys Lys Phe Lys Glu
      145              150              155              160

Lys Gly Ile Asn Val Glu Asn Asp Ala Leu Glu Tyr Leu Leu Gln Leu
      165              170              175

Thr Gly Tyr Asn Leu Met Glu Leu Lys Leu Glu Val Glu Lys Leu Ile
      180              185              190

Asp Tyr Ala Ser Glu Lys Lys Ile Leu Thr Leu Asp Glu Val Lys Arg
      195              200              205

Val Ala Phe Ser Val Ser Glu Asn Val Asn Val Phe Glu Phe Val Asp
      210              215              220

Leu Leu Leu Leu Lys Asp Tyr Glu Lys Ala Leu Lys Val Leu Asp Ser
      225              230              235              240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
      245              250              255

Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
      260              265              270

Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
      275              280              285

```

Sequence_Listing_R10901_Corrected.txt

Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
290 295 300

Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
305 310 315 320

Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
325 330 335

Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
340 345 350

<210> 125

<211> 1051

<212> DNA

<213> Aquifex aeolicus

<400> 125

```
atggaaaaaag ttttttttggg aaaaactccag aaaaccttgc acatacccgaggactcctt 60
ttttacggca aagaaggaag cggaaagacg aaaacagctt ttgaatttgc aaaaggtatt 120
ttatgtaagg aaaacgtacc tggggatgcg gaagttgtcc ctctgcaaa cacgtaaagc 180
agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
cggtaaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
gagcggacat tacataaaga tagaacagat aaggggaagt aagaactttg cctatgtgaa 360
gcccgcacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
ggcggcaaac gctcttttaa aggtatttga agagccacct gcggacacca cctttatctt 480
gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtga 540
gttcaaggcg ttttcagtaa aagaggttat ggaaatagcg aaagtagacg aggaaatagc 600
gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca aagatatcct 660
aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattgg 780
atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
actctttaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
cggtcaggcg gattaataaa ccgttattga ttccgtaaca tttaaaccct aatctaaatt 960
atgagagcct ttgaaggagg tctggtatgg aaaatttgaa gattagatat atagatacga 1020
ggaagatagg aaccgtgagc ggtgtaaaag t 1051
```

<210> 126

<211> 305

<212> PRT

<213> Aquifex aeolicus

<400> 126

```
Met Glu Lys Val Phe Leu Glu Lys Leu Gln Lys Thr Leu His Ile Pro
  1 5 10 15
Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr
 20 25 30
Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp
 35 40 45
Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu
 50 55 60
Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys
 65 70 75 80
```


Sequence_Listing_R10901_Corrected.txt

```

Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe
      85                      90                      95
Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg
      100                      105                      110
Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys
      115                      120                      125
Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn
      130                      135                      140
Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile
      145                      150                      155                      160
Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg
      165                      170                      175
Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu
      180                      185                      190
Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu
      195                      200                      205
Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val
      210                      215                      220
Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
      225                      230                      235                      240
Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile
      245                      250                      255
Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
      260                      265                      270
Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
      275                      280                      285
Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
      290                      295                      300

```

Asp
305

<210> 127
<211> 630
<212> DNA
<213> Aquifex aeolicus

```

<400> 127
atgaacttcc tgaaaaagtt ctttttactg agaaaagctc aaaagtctcc ttacttcgaa 60
gagttctacg aagaaatcga tttgaaccag aaggtgaaag atgcaagggt ttagtatttt 120
gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcggtt 180
gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgac 240
gagataaagg cggcggagat acatggaata accagggaag acgttgaaaa gtacggaaag 300
gaaccaaagg aagtaatatata cgactttctg aagtacataa agggaagcgt tctcgttggc 360

```

Sequence_Listing_R10901_Corrected.txt

```
tactacgtga agtttgacgt ctcactcggt gagaagtact ccataaagta cttccagtat 420
ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
aggagtcttg acgaccttat gaaggaaactc ggtgtagaaa taagggaag gcacaacgcc 540
cttgaagatg cctacataac cgctcttctt ttcctaaagt acgtttaccc gaacagggag 600
tacagactaa aggatctccc gattttcctt                                     630
```

<210> 128

<211> 210

<212> PRT

<213> Aquifex aeolicus

<400> 128

```
Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser
  1                      5                      10                      15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val
          20          25          30

Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp
          35          40          45

Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn
          50          55          60

Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp
          65          70          75          80

Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu
          85          90          95

Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr
          100          105          110

Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser
          115          120          125

Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn
          130          135          140

Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly
          145          150          155          160

Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala
          165          170          175

Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu
          180          185          190

Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile
          195          200          205

Phe Leu
          210
```

<210> 129

<211> 526

<212> DNA

Sequence_Listing_R10901_Corrected.txt

<213> Aquifex aeolicus

<400> 129

```

atgctcaata aggttttttat aataggaaga cttacgggtg accccggtat aacttatcta 60
cagagcgga cgcgcgtagt agagtttact ctggccttaca acagaaggta taaaaaccag 120
aacgggtgaat ttcaggagga aagtcacttc ttgacgtaa aggcgtacgg aaaaatggct 180
gaagactggg ctacacgctt ctcgaaagga tacctcgtac tcgtagaggg aagactctcc 240
caggaaaagt gggagaaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaagggtgt gaacttcaag cagaagaaga ggaggaagtt 360
cctcccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccctt ttaattttga ggagggttaa gtatggtagt gagagctcct 480
aagaagaaaag ttgttatgta ctgtgaacaa aagagagagc cagatt 526

```

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus

<400> 130

```

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
  1             5             10             15

```

```

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
             20             25             30

```

```

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
      35             40             45

```

```

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
      50             55             60

```

```

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
      65             70             75             80

```

```

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
      85             90             95

```

```

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
      100            105            110

```

```

Gln Ala Glu Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
      115            120            125

```

```

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
      130            135            140

```

```

Ile Pro Phe
145

```

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

```

atgcaatttg tggataaaact tccctgtgac gaatccgccg agagggcggt tcttggcagt 60
atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaaga agaagacttc 120

```

Sequence_Listing_R10901_Corrected.txt

```

tgcataagacg agcacaagct actttttcagg gttctttacaa acctctgggtc cgagtacggc 180
aataagctcgc atttcgtatt aataaaggat cactttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatccctga cacgcttgag 300
gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaactcattc acaaaggaaa ggaatacaaa gactttcaca cattaatcga ggaagcccag 420
agcaggatat tttccatagc ggaaagtgc acatctacgc agttttacca tgtgaaagac 480
gttgcggaag aagttataga actcatttat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggtttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600
ttaataatac tcgcgcgaag acccgggtatg gggaaaaccg cctttatgct ctccataatc 660
tacaatctcg caaaagacga gggaaaaccc tcagctgtat tttccttgga aatgagcaag 720
gaacagctcg ttatgagaat cctctctatg atgtcggagg tcccaacttt caagataagg 780
tctggaagta tatcgaaatg agatttaaa aagcttgaag caagcgcaat agaactcgca 840
aagtaagaca tatacctcga cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaagc tcagaaagga aaaggaagtt gaggctcgtg cgggtggacta cttgcaactt 960
ctgagaccgc cagtcgcaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgogca gctctcccgt 1080
gaggtgaaa agaggagtga taaaagaccc cagcttgogg acctcagaga atccggacag 1140
atagaacagg acgcagacct aatccttttc ctccacagac ccgagtacta caagaaaaag 1200
ccaaatcccg aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattg tgaagctcgc atttattaag gactacacta agtttgcaaa cctagaagcc 1320
cttcctgaac aacotcctga agaagaggaa ctttcgcaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472

```

<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

```

Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
 1             5             10             15

Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
 20             25             30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
 35             40             45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
 50             55             60

Phe Val Leu Ile Lys Asp His Leu Glu Lys Lys Asn Leu Leu Gln Lys
 65             70             75             80

Ile Pro Ile Asp Trp Leu Glu Glu Leu Tyr Glu Glu Ala Val Ser Pro
 85             90             95

Asp Thr Leu Glu Glu Val Cys Lys Ile Val Lys Gln Arg Ser Ala Gln
100            105            110

Arg Ala Ile Ile Gln Leu Gly Ile Thr Ser Thr Gln Phe Tyr His Val
115            120            125

Lys Asp Val Ala Glu Glu Val Ile Glu Leu Ile Tyr Lys Phe Lys Ser
130            135            140

Ser Asp Arg Leu Val Thr Gly Leu Pro Ser Gly Phe Thr Glu Leu Asp

```

Sequence_Listing_R10901_Corrected.txt

```

145          150          155          160
Leu Lys Thr Thr Gly Phe His Pro Gly Asp Leu Ile Ile Leu Ala Ala
      165          170          175
Arg Pro Gly Met Gly Lys Thr Ala Phe Met Leu Ser Ile Ile Tyr Asn
      180          185          190
Leu Ala Lys Asp Glu Gly Lys Pro Ser Ala Val Phe Ser Leu Glu Met
      195          200          205
Ser Lys Glu Gln Leu Val Met Arg Leu Leu Ser Met Met Ser Glu Val
      210          215          220
Pro Leu Phe Lys Ile Arg Ser Gly Ser Ile Ser Asn Glu Asp Leu Lys
      225          230          235          240
Lys Leu Glu Ala Ser Ala Ile Glu Leu Ala Lys Tyr Asp Ile Tyr Leu
      245          250          255
Asp Asp Thr Pro Ala Leu Thr Thr Thr Asp Leu Arg Ile Arg Ala Arg
      260          265          270
Lys Leu Arg Lys Glu Lys Glu Val Glu Phe Val Ala Val Asp Tyr Leu
      275          280          285
Gln Leu Leu Arg Pro Pro Val Arg Lys Ser Ser Arg Gln Glu Glu Val
      290          295          300
Ala Glu Val Ser Arg Asn Leu Lys Ala Leu Ala Lys Glu Leu His Ile
      305          310          315          320
Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser
      325          330          335
Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
      340          345          350
Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
      355          360          365
Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
      370          375          380
Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
      385          390          395          400
Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
      405          410          415
Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly
      420          425          430
Phe Glu Asp Ile Asp Phe
      435

```

<210> 133

<211> 1526

Sequence_Listing_R10901_Corrected.txt

<212> DNA

<213> Aquifex aeolicus

<400> 133

```

atgtcctcgg acatagacga acttagacgg gaaatagata tagtagacgt catttcogaa 60
tacttaaaact tagagaaggt aggttccaat tacagaacga actgtccctt tcacootgac 120
gatacacccct ccttttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgcggg 180
gtaggggggag acgcgataaa gttcgtttcc ctttacgagg acatctccta ttttgaagcc 240
gcccttgaac tcgcaaaacg ctacggaaaag aaattagacc ttgaaaagat atcaaaagac 300
gaaaaggtat acgtggctct tgacagggtt tgtgatttct acagggaaag cctttotcaaa 360
aacagagagg caagtgahta cgtaaagagt aggggaatag accotaaagt agcgaggaag 420
tttgatcttg ggtacgcacc ttccagtga gactcgttaa aagtcttaaa agagaacgat 480
cttttagagg cttaccttga aactaaaaac ctcttttctc ctacgaaggg tgtttacagg 540
gatctctttc ttccggcgtgt cgtgatcccg ataaaggatc cgaggggaag agttataggt 600
ttcgggtggaa ggaggatagt agaggacaaa tctcccaagt acataaactc tccagacagc 660
agggatattt aaaaggggga gaacttatto ggtctttacg aggcaaagga gtatataaag 720
gaagaaggat ttgcgatact tgtggaaggg taactttgacc ttttgagact tttttccgag 780
ggaataagga acgttggttg accctcgggt acagccctga cccaaaatca ggcaaacctc 840
ctttccaagt tcacaaaaaa ggtctacatc ctttacgaag gagatgatgc gggaagaaag 900
gctatgaaaa gtgccattcc cctactctc agtgcaggag tggaaagttt tcccgtttac 960
ctccccgaag gatacgatcc cgacgagttt ataaaggatc tcgggaaaga ggaattaaga 1020
agactgataa acagctcagg ggagctcttt gaaacgctca taaaaaccgc aagggaaaac 1080
ttagaggaga aaacgcgtga gttcaggtat tatctgggtt ttatttccga tggagtaagg 1140
cgctttgctc tggcttcgga gtttcacacc aagtacaaag ttcttatgga aattttatta 1200
atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac tctcttttaa ggaaaaaatc 1260
ttcctgaaag gactgataga attaaaacca aaaatagacc ttgaagtctt gaacttaagt 1320
cctgagttaa aggaactcgc agttaacgcc ttaaacggag aggagcattt acttccaaaa 1380
gaagttctcg agtaccaggt ggataacttg gagaaacttt ttaacaacat ccttagggat 1440
ttacaaaaat ctgggaaaaa gaggaagaaa agagggttga aaaatgtaaa tacttaatta 1500
actttaataa atttttagag ttagga 1526

```

<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

```

Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
 1             5             10             15

Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
 20             25             30

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
 35             40             45

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
 50             55             60

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
 65             70             75             80

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
 85             90             95

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
100            105            110

```

Sequence_Listing_R10901_Corrected.txt

```

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
 115                               120                               125

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
 130                               135                               140

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
 145                               150                               155                               160

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys
                               165                               170                               175

Gly Val Tyr Arg Asp Leu Phe Leu Arg Arg Val Val Ile Pro Ile Lys
                               180                               185                               190

Asp Pro Arg Gly Arg Val Ile Gly Phe Gly Gly Arg Arg Ile Val Glu
                               195                               200                               205

Asp Lys Ser Pro Lys Tyr Ile Asn Ser Pro Asp Ser Arg Val Phe Lys
 210                               215                               220

Lys Gly Glu Asn Leu Phe Gly Leu Tyr Glu Ala Lys Glu Tyr Ile Lys
 225                               230                               235                               240

Glu Glu Gly Phe Ala Ile Leu Val Glu Gly Tyr Phe Asp Leu Leu Arg
                               245                               250                               255

Leu Phe Ser Glu Gly Ile Arg Asn Val Val Ala Pro Leu Gly Thr Ala
                               260                               265                               270

Leu Thr Gln Asn Gln Ala Asn Leu Leu Ser Lys Phe Thr Lys Lys Val
                               275                               280                               285

Tyr Ile Leu Tyr Asp Gly Asp Asp Ala Gly Arg Lys Ala Met Lys Ser
 290                               295                               300

Ala Ile Pro Leu Leu Leu Ser Ala Gly Val Glu Val Tyr Pro Val Tyr
 305                               310                               315                               320

Leu Pro Glu Gly Tyr Asp Pro Asp Glu Phe Ile Lys Glu Phe Gly Lys
                               325                               330                               335

Glu Glu Leu Arg Arg Leu Ile Asn Ser Ser Gly Glu Leu Phe Glu Thr
                               340                               345                               350

Leu Ile Lys Thr Ala Arg Glu Asn Leu Glu Glu Lys Thr Arg Glu Phe
                               355                               360                               365

Arg Tyr Tyr Leu Gly Phe Ile Ser Asp Gly Val Arg Arg Phe Ala Leu
 370                               375                               380

Ala Ser Glu Phe His Thr Lys Tyr Lys Val Pro Met Glu Ile Leu Leu
 385                               390                               395                               400

Met Lys Ile Glu Lys Asn Ser Gln Glu Lys Glu Ile Lys Leu Ser Phe
                               405                               410                               415

Lys Glu Lys Ile Phe Leu Lys Gly Leu Ile Glu Leu Lys Pro Lys Ile
 420                               425                               430

```

Sequence_Listing_R10901_Corrected.txt

Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val
435 440 445

Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu
450 455 460

Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp
465 470 475 480

Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val
485 490 495

Asn Thr

<210> 135

<211> 705

<212> DNA

<213> Aquifex aeolicus

<400> 135

```
atgcaagata ccgctacctg cagtatttgt caggggacgg gattcgtaaa gaccgaagac 60
aacaaggtaa ggctctgcga atgcagggtc aagaaaaggg atgtaaacag ggaactaaac 120
atcccaaaga ggtactggaa cgccaactta gacacttacc accccaagaa cgtatcccag 180
aacagggcac ttttgacgat aagggtcttc gtccacaact tcaatcccga ggaagggaaa 240
gggcttacct ttgtaggatc tcctggagtc ggcaaaaactc accttgcggt tgcaacatta 300
aaagcgattt atgagaagaa gggaatcaga ggatacttct tcgatacgaa ggatctaata 360
ttcagggtta aacacttaat ggacgagga aaggatacaa agtttttaaa aactgtctta 420
aactcaccgg ttttggttct cgacgacctc ggttctgaga ggctcagtga ctggcagagg 480
gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600
agcagactcg gagaaaacgt agtttcaaaa atttacgaga tgaacgagtt gctcgttata 660
aagggttcog acctcaggaa gtctaaaaag ctatcaaccc catct 705
```

<210> 136

<211> 235

<212> PRT

<213> Aquifex aeolicus

<400> 136

Met Gln Asp Thr Ala Thr Cys Ser Ile Cys Gln Gly Thr Gly Phe Val
1 5 10 15

Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys
20 25 30

Arg Asp Val Asn Arg Glu Leu Asn Ile Pro Lys Arg Tyr Trp Asn Ala
35 40 45

Asn Leu Asp Thr Tyr His Pro Lys Asn Val Ser Gln Asn Arg Ala Leu
50 55 60

Leu Thr Ile Arg Val Phe Val His Asn Phe Asn Pro Glu Glu Gly Lys
65 70 75 80

Gly Leu Thr Phe Val Gly Ser Pro Gly Val Gly Lys Thr His Leu Ala

Sequence_Listing_R10901_Corrected.txt

85

90

95

Val Ala Thr Leu Lys Ala Ile Tyr Glu Lys Lys Gly Ile Arg Gly Tyr
 100 105 110

Phe Phe Asp Thr Lys Asp Leu Ile Phe Arg Leu Lys His Leu Met Asp
 115 120 125

Glu Gly Lys Asp Thr Lys Phe Leu Lys Thr Val Leu Asn Ser Pro Val
 130 135 140

Leu Val Leu Asp Asp Leu Gly Ser Glu Arg Leu Ser Asp Trp Gln Arg
 145 150 155 160

Glu Leu Ile Ser Tyr Ile Ile Thr Tyr Arg Tyr Asn Asn Leu Lys Ser
 165 170 175

Thr Ile Ile Thr Thr Asn Tyr Ser Leu Gln Arg Glu Glu Glu Ser Ser
 180 185 190

Val Arg Ile Ser Ala Asp Leu Ala Ser Arg Leu Gly Glu Asn Val Val
 195 200 205

Ser Lys Ile Tyr Glu Met Asn Glu Leu Leu Val Ile Lys Gly Ser Asp
 210 215 220

Leu Arg Lys Ser Lys Lys Leu Ser Thr Pro Ser
 225 230 235

<210> 137

<211> 4101

<212> DNA

<213> *Thermatoga maritima*

<400> 137

atgaaaaaga ttgaaaattt gaagtggaaa aatgtctcgt ttaaaagcct ggaaatagat 60
 cccgatgcag gtgtggttct cgtttccgtg gaaaaattct ccgaagagat agaagacctt 120
 gtgogttttac tggagaagaa gacgcggttt cgagtcacgt tgaacggtgt tcaaaaaagt 180
 aacgggggac taaggggaaa gatactttcc cttctcaacg gtaatgtgcc ttacataaaa 240
 gatgttggtt tcgaaggaaa caggctgatt ctgaaagtgc ttggagattt cgcgcgggac 300
 aggatcgctt ccaaactcag aagcacgaaa aaacagctcg atgaactgct gcctcccga 360
 acagagatca tgctggaggt tgtggagcct ccggaagatc ttttgaaaaa ggaagtacca 420
 caaccagaaa agagagaaga accaaagggt gaagaattga agatcgagga tgaanaaccac 480
 atctttggac agaaaaccag aaagatcgtc ttcaccccct caaaaatctt tgagtacaac 540
 aaaaagacat cgggtgaagg caagatcttc aaaatagaga agatcgaggg gaaaagaacg 600
 gtcccttctga ttacctgac agacggagaa gattctctga tctgcaaagt cttcaacgac 660
 gttgaaaaag tcgaagggaa agtatcgggt ggagacgtga tcgttgccac aggagacctc 720
 cttctcgaaa aocggggagcc caccctttac gtgaagggaa tcacaaaact tcccgaagcg 780
 aaaaggatgg acaaatctcc ggttaagagg gtggagctcc acgcccatac caagttcagc 840
 gatcaggacg caataacaga tgtgaacgaa tatgtgaaac gagccaagga atggggcttt 900
 ccgcgatag cctcacgga tcatgggaac gttcaggcca taccttactt ctacgacgcg 960
 gcgaaagaag ctggaataaa gcccatthtc ggtatcgaag cgtatctggt gagtgcgtg 1020
 gagcccgta taaggaatct ctccgacgat tcgacgtttg gagatgccac gttcgtcgtc 1080
 ctcgacttcg agacgacggg tctcgaccog caggtggatg agatcatcga gataggagcg 1140
 gtgaagatac aggttgccca gatagtggac gagtaccaca ctctcataaa gccttcagg 1200
 gagatctcaa gaaaaagttc ggagatcacc ggaatcactc aagagatgct ggaaaacaag 1260
 agaagcatcg aggaagtctt gccggagtgc ctcggttttc tggaagattc catcatcgta 1320
 gcacacaacg ccaacttcga ctacagattt ctgaggctgt ggatcaaaaa agtgcgtgga 1380

Sequence_Listing_R10901_Corrected.txt

```

ttggactggg aaagacccta catagatacg ctgcgcctcg caaagtccct tctcaaactg 1440
agaagctact ctctggattc cgttgtggaa aagctcggat tgggtccctt cgggcaccac 1500
agggccctgg atgaacggag ggtcacccgt cagggtttcc tcagggttcgt tgagatgatg 1560
aagaagatcg gtatcacgaa gctttcagaa atggagaagt tgaaggatac gatagactac 1620
accgcgttga aacccttcca ctgcacgata ctcggttcaga acaaaaaggg attgaaaaac 1680
ctatacaaac tggttttctga ttcttatata aagtacttct acggtgttcc gaggatcctc 1740
aaaagtgagc tcatcgagaa cagagaagga ctgctcgtgg gtagcgcgtg tatctccggt 1800
gagctcggac gtgcgcgcct cgaaggagcg agtgattcag aactcgaaga gatcgcgaag 1860
ttctacgact acatagaagt actgcgcctc gacgttatag ccgaagatga agaagacctc 1920
gacagagaaa gactgaaaag atgtgtaccg aaactctaca gaatagcgaa aaaattgaac 1980
aagttcgtcg tcatgacccg tgatgttcat ttctctgata ccgaagatgc caggggcaga 2040
gctgcacttc tggcacctca gggaaaacaga aacttcgaga atcagccgcg actctacctc 2100
agaacgaccg aagaaatgct cgagaaggcg atagagatat tcgaagatga agagatcgcg 2160
agggaagtcg tgatagagaa tcccaacaga atagccgata tgatcgagga agtgcagccg 2220
ctcgagaaaa aacttcaccc gccgatcata gagaacgcgc atgaaatagt gagaaaacctc 2280
accatgaagc gggcgtagca gatctacggt gatccgcttc ccgaaatcgt ccagaagcgt 2340
gtggaaaagg aactgaacgc catcataaat catggatacg ccgtttctca tctcatcgct 2400
caggagctcg ttcagaaatc tatgagcgat gggttacgtgg ttggatccag aggatccgtc 2460
gggtcttccg tcgtggccaa tctcctcgga ataacagagg tgaatccct accaccacat 2520
tacagggtgc cagagtgcaa atactttgaa gttgtcgaag acgacagata cggagcgggt 2580
taacgacctc ccaacaagaa ctgtccaaga tgtggggctc ctctcagaaa agacggccac 2640
ggcataccgt ttgaaacggt catgggggtc gaggtgaca aggtccccga catagatctc 2700
aacttctcag gagagtatca ggaacgtgct catcgttttg tggaaagaact cttcggtaaa 2760
gaccacgtct atagggcggg aaccataaac accatcgcg aaagaagtgc ggtgggttac 2820
gtgagaagct acgaagagaa aaccggaaag aagctcagaa aggcggaaat ggaaagactc 2880
gtttccatga tcacgggagt gaagagaacg acgggtcagc acccagggg gctcatgatc 2940
ataccgaaaag acaaagaagt ctacgatttc actcccatac agtatccagc caacgataga 3000
aacgcagggtg tgttcaccac gcacttcgca tacgagacga tccatgatga cctggtgaag 3060
atagatgcgc tcggccacga tgatccact ttcatacaga tgctcaagga cctcaccgga 3120
atcgatccca tgacgattcc catggatgac cccgatacgc tcgccataat cagttctgtg 3180
aagcctcttg gtgtggatcc cgttgagctg gaaagcgatg tgggaacgta cggaaattccg 3240
gagttcggaa ccgagtttgt gaggggaatg ctcggtgaaa cgagaccaa gagtttcgcc 3300
gagcttgtga gaatctcagg actgtcacac ggtacggacg tctggttgaa caacgcacgt 3360
gatttgataa acctcggcta cgccaagctc tccgaggtta tctcgtgtag ggaacacatc 3420
atgaacttcc tcatacacaa aggaatggaa ccgtcacttg ccttcaagat catggaaaac 3480
gtcaggaagg gaaaggggtat cacagaagag atggagagcg agatgagaag gctgaagggt 3540
ccagaatggt tcacgaatc ctgtaaaagg atcaaatatc tcttcccgaa agctcacgct 3600
gtggttacg tgagtatggc cttcagaatt gcttacttca aggttcaact tctcttcag 3660
ttttacgcgg cgtacttcac gataaaaggt gatcagttcg atccggttct cgtactcagg 3720
ggaaaagaag ccataaaagag gcgcttgaga gaactcaaag cgatgcctgc caaagacgcc 3780
cagaagaaaa acgaagtgaq tgttctggag gttgccttg aaatgatact gagaggtttt 3840
tccttctac cgcccgacat cttcaaatcc gacgcgaaga aatttctgat agaaggaaac 3900
tcgctgagaa ttccgttcaa caaacttcca ggaactgggt acagcgttgc cgagtcgata 3960
atcagagcca gggaagaaaa gccgttcaact tcggtggaag atctcatgaa gaggaccaag 4020
gtcaacaaaa atcacataga gctgatgaaa agcctgggtg ttctcgggga ccttcagag 4080
acggaacagt tcacgctttt c

```

<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

Met Lys Lys Ile Glu Asn Leu Lys Trp Lys Asn Val Ser Phe Lys Ser
1 5 10 15

Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
20 25 30

Sequence_Listing_R10901_Corrected.txt

```

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
   35                               40                               45

Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
   50                               55                               60

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
   65                               70                               75                               80

Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
   85                               90                               95

Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln
  100                               105                               110

Leu Asp Glu Leu Leu Pro Pro Gly Thr Glu Ile Met Leu Glu Val Val
  115                               120                               125

Glu Pro Pro Glu Asp Leu Leu Lys Lys Glu Val Pro Gln Pro Glu Lys
  130                               135                               140

Arg Glu Glu Pro Lys Gly Glu Glu Leu Lys Ile Glu Asp Glu Asn His
  145                               150                               155                               160

Ile Phe Gly Gln Lys Pro Arg Lys Ile Val Phe Thr Pro Ser Lys Ile
  165                               170                               175

Phe Glu Tyr Asn Lys Lys Thr Ser Val Lys Gly Lys Ile Phe Lys Ile
  180                               185                               190

Glu Lys Ile Glu Gly Lys Arg Thr Val Leu Leu Ile Tyr Leu Thr Asp
  195                               200                               205

Gly Glu Asp Ser Leu Ile Cys Lys Val Phe Asn Asp Val Glu Lys Val
  210                               215                               220

Glu Gly Lys Val Ser Val Gly Asp Val Ile Val Ala Thr Gly Asp Leu
  225                               230                               235                               240

Leu Leu Glu Asn Gly Glu Pro Thr Leu Tyr Val Lys Gly Ile Thr Lys
  245                               250                               255

Leu Pro Glu Ala Lys Arg Met Asp Lys Ser Pro Val Lys Arg Val Glu
  260                               265                               270

Leu His Ala His Thr Lys Phe Ser Asp Gln Asp Ala Ile Thr Asp Val
  275                               280                               285

Asn Glu Tyr Val Lys Arg Ala Lys Glu Trp Gly Phe Pro Ala Ile Ala
  290                               295                               300

Leu Thr Asp His Gly Asn Val Gln Ala Ile Pro Tyr Phe Tyr Asp Ala
  305                               310                               315                               320

Ala Lys Glu Ala Gly Ile Lys Pro Ile Phe Gly Ile Glu Ala Tyr Leu
  325                               330                               335

Val Ser Asp Val Glu Pro Val Ile Arg Asn Leu Ser Asp Asp Ser Thr

```

Sequence_Listing_R10901_Corrected.txt

340		345		350
Phe Gly Asp Ala Thr Phe Val Val Leu Asp Phe Glu Thr Thr Gly Leu	355	360	365	
Asp Pro Gln Val Asp Glu Ile Ile Glu Ile Gly Ala Val Lys Ile Gln	370	375	380	
Gly Gly Gln Ile Val Asp Glu Tyr His Thr Leu Ile Lys Pro Ser Arg	385	390	395	400
Glu Ile Ser Arg Lys Ser Ser Glu Ile Thr Gly Ile Thr Gln Glu Met	405	410	415	
Leu Glu Asn Lys Arg Ser Ile Glu Glu Val Leu Pro Glu Phe Leu Gly	420	425	430	
Phe Leu Glu Asp Ser Ile Ile Val Ala His Asn Ala Asn Phe Asp Tyr	435	440	445	
Arg Phe Leu Arg Leu Trp Ile Lys Lys Val Met Gly Leu Asp Trp Glu	450	455	460	
Arg Pro Tyr Ile Asp Thr Leu Ala Leu Ala Lys Ser Leu Leu Lys Leu	465	470	475	480
Arg Ser Tyr Ser Leu Asp Ser Val Val Glu Lys Leu Gly Leu Gly Pro	485	490	495	
Phe Arg His His Arg Ala Leu Asp Asp Ala Arg Val Thr Ala Gln Val	500	505	510	
Phe Leu Arg Phe Val Glu Met Met Lys Lys Ile Gly Ile Thr Lys Leu	515	520	525	
Ser Glu Met Glu Lys Leu Lys Asp Thr Ile Asp Tyr Thr Ala Leu Lys	530	535	540	
Pro Phe His Cys Thr Ile Leu Val Gln Asn Lys Lys Gly Leu Lys Asn	545	550	555	560
Leu Tyr Lys Leu Val Ser Asp Ser Tyr Ile Lys Tyr Phe Tyr Gly Val	565	570	575	
Pro Arg Ile Leu Lys Ser Glu Leu Ile Glu Asn Arg Glu Gly Leu Leu	580	585	590	
Val Gly Ser Ala Cys Ile Ser Gly Glu Leu Gly Arg Ala Ala Leu Glu	595	600	605	
Gly Ala Ser Asp Ser Glu Leu Glu Glu Ile Ala Lys Phe Tyr Asp Tyr	610	615	620	
Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu	625	630	635	640
Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala	645	650	655	

Sequence_Listing_R10901_Corrected.txt

```

Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu
660                      665                      670

Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly
675                      680                      685

Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu
690                      695                      700

Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala
705                      710                      715                      720

Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu
725                      730                      735

Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn
740                      745                      750

Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile
755                      760                      765

Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu
770                      775                      780

Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala
785                      790                      795                      800

Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser
805                      810                      815

Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr
820                      825                      830

Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr
835                      840                      845

Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro
850                      855                      860

Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His
865                      870                      875                      880

Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro
885                      890                      895

Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg
900                      905                      910

Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr
915                      920                      925

Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr
930                      935                      940

Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu
945                      950                      955                      960

Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly
965                      970                      975

```

Sequence_Listing_R10901_Corrected.txt

Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro
980 985 990

Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His
995 1000 1005

Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu
1010 1015 1020

Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly
1025 1030 1035 1040

Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile
1045 1050 1055

Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser
1060 1065 1070

Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg
1075 1080 1085

Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg
1090 1095 1100

Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg
1105 1110 1115 1120

Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys
1125 1130 1135

Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser
1140 1145 1150

Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr
1155 1160 1165

Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe
1170 1175 1180

Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala
1185 1190 1195 1200

Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His
1205 1210 1215

Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln
1220 1225 1230

Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg
1235 1240 1245

Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn
1250 1255 1260

Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe
1265 1270 1275 1280

Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu

Sequence_Listing_R10901_Corrected.txt

1285

1290

1295

Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu
 1300 1305 1310

Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro
 1315 1320 1325

Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn
 1330 1335 1340

His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu
 1345 1350 1355 1360

Thr Glu Gln Phe Thr Leu Phe
 1365

<210> 139

<211> 567

<212> DNA

<213> *Thermatoga maritima*

<400> 139

```

gtgctcgcca tgatatggaa cgacaccgtt ttttgcgtcg tagacacaga aaccacggga 60
accgatccct ttgccggaga ccggatagtt gaaatagccg ctgttcctgt cttcaagggg 120
aagatctaca gaaacaaagc gtttcaactc ctcgtgaatc ccagaataag aatccctgcg 180
ctgattcaga aagttcacgg tatcagcaac atggacatcg tgggaagcgc agacatggac 240
acagtttacg atcttttcag ggattacgtg aagggaacgg tgctcgtgtt tcacaacgcc 300
aacttcgacc tcacttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360
aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcattctctc 420
aaatggctct ccgaaagact tggaataaaa accacgatac ggcaccgtgc tcttccagat 480
gccctgggtga ccgcaagagt ttttgtgaag cttgttgaat ttcttgggtga aaacagggtc 540
aacgaattca tacgtggaaa acggggg 567

```

<210> 140

<211> 189

<212> PRT

<213> *Thermatoga maritima*

<400> 140

Met Leu Ala Met Ile Trp Asn Asp Thr Val Phe Cys Val Val Asp Thr
 1 5 10 15

Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
 20 25 30

Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
 35 40 45

His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
 50 55 60

Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
 65 70 75 80

Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
 85 90 95

Sequence_Listing_R10901_Corrected.txt

Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
100 105 110

Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
115 120 125

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
180 185

<210> 141

<211> 1434

<212> DNA

<213> *Thermatoga maritima*

<400> 141

```
gtggaagttc tttacaggaa gtacaggcca aagacttttt ctgaggttgt caatcaggat 60
catgtgaaga aggcaataat cgggtgctatt cagaagaaca gcgtggccca cggatacata 120
ttcgccggtc cgaggggaac ggggaagact actcttgcca gaattctcgc aaaatccctg 180
aactgtgaga acagaaaagg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
gacgagggaa ccttcattga cgtgatagag ctcgacggcg cctccaacag aggaatagac 300
gagatcagaa gaatcagaga cgccgttggg tacaggccga tggaaggtaa atacaaagtc 360
tacataatag acgaagtcca catgctcacg aaagaagcct tcaacgcgct cctcaaaaca 420
ctcgaagaac ctccctccca cgtcgtgttc gtgctggcaa cgacaaacct tgagaagggt 480
cctcccacga ttatctcgag atgtcagggt ttcgagttca gaaacattcc cgacgagctc 540
atcgaaaaga ggctccagga agttgcggag gctgaaggaa tagagataga cagggaagct 600
ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgctcac catgctcgag 660
caggtgtgga agttctcgga aggaaagata gatctcgaga cggtagacag ggcgctcggg 720
ttgataccga tacagggtgt tcgcgattac gtgaacgcta tcttttctgg tgatgtgaaa 780
agggctctta ccgttctcga cgacgtctat tacagcggga aggactacga ggtgctcatt 840
caggaagcag tcgaggatct ggtcgaagac ctggaaaggg agagaggggt ttaccagggt 900
tcagcgaacg ataatgttca ggtttcgaga caacttctga atcttctgag agagataaag 960
ttcgccgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgaggttc 1020
tccaccacaa acgttcagga aaaagatgtc agagaaaaaa acgataatto aaatgtacag 1080
cagaaagaag agaagaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgag 1140
ttcgagaaac gtttcaaaga actcatggaa gaactgaaag aaaagggcga tctctctatc 1200
tttgctcgctc tcagcctctc agaggtgcag tttgacggag aaaaggtgat tatttctttt 1260
gattcatcga aagctatgca ttacgagttg atgaagaaaa aactgcctga gctggaaaaa 1320
attttttcta gaaaactcgg gaaaaaagta gaagttgaac ttcgactgat gggaaaagaa 1380
gaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga ggga 1434
```

<210> 142

<211> 478

<212> PRT

<213> *Thermatoga maritima*

<400> 142

Met Glu Val Leu Tyr Arg Lys Tyr Arg Pro Lys Thr Phe Ser Glu Val

Sequence_Listing_R10901_Corrected.txt

1	5	10	15
Val Asn Gln Asp His Val Lys Lys Ala Ile Ile Gly Ala Ile Gln Lys	20	25	30
Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly	35	40	45
Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn	50	55	60
Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile	65	70	75
Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn	85	90	95
Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg	100	105	110
Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met	115	120	125
Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro	130	135	140
Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val	145	150	155
Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile	165	170	175
Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu	180	185	190
Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala	195	200	205
Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys	210	215	220
Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly	225	230	235
Leu Ile Pro Ile Gln Val Val Arg Asp Tyr Val Asn Ala Ile Phe Ser	245	250	255
Gly Asp Val Lys Arg Val Phe Thr Val Leu Asp Asp Val Tyr Tyr Ser	260	265	270
Gly Lys Asp Tyr Glu Val Leu Ile Gln Glu Ala Val Glu Asp Leu Val	275	280	285
Glu Asp Leu Glu Arg Glu Arg Gly Val Tyr Gln Val Ser Ala Asn Asp	290	295	300
Ile Val Gln Val Ser Arg Gln Leu Leu Asn Leu Leu Arg Glu Ile Lys	305	310	315
			320

Sequence_Listing_R10901_Corrected.txt

Phe Ala Glu Glu Lys Arg Leu Val Cys Lys Val Gly Ser Ala Tyr Ile
325 330 335

Ala Thr Arg Phe Ser Thr Thr Asn Val Gln Glu Asn Asp Val Arg Glu
340 345 350

Lys Asn Asp Asn Ser Asn Val Gln Gln Lys Glu Glu Lys Lys Glu Thr
355 360 365

Val Lys Ala Lys Glu Glu Lys Gln Glu Asp Ser Glu Phe Glu Lys Arg
370 375 380

Phe Lys Glu Leu Met Glu Glu Leu Lys Glu Lys Gly Asp Leu Ser Ile
385 390 395 400

Phe Val Ala Leu Ser Leu Ser Glu Val Gln Phe Asp Gly Glu Lys Val
405 410 415

Ile Ile Ser Phe Asp Ser Ser Lys Ala Met His Tyr Glu Leu Met Lys
420 425 430

Lys Lys Leu Pro Glu Leu Glu Asn Ile Phe Ser Arg Lys Leu Gly Lys
435 440 445

Lys Val Glu Val Glu Leu Arg Leu Met Gly Lys Glu Glu Thr Ile Glu
450 455 460

Lys Val Ser Gln Lys Ile Leu Arg Leu Phe Glu Gln Glu Gly
465 470 475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

```
atgaaagtaa ccgtcacgac tcttgaattg aaagacaaaa taaccatcgc ctcaaaagcg 60
ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aatttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggta ccaggagatg tcattcagaa gatggtoaag 240
gttctccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagtctt 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttcaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat gggtgaaaag 420
gtcatcttgc cgcgtgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatggtt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
agggtttctc tgcgacaaa tgatgtagaa acggtgatga gagtggatga cgtgaattt 720
cccgattaca aaagggtgat ccccgaaact ttcaaaacga aagtgggtgt ttccagaaaa 780
gaactcaggg aatctttgaa gagggtgatg gtgattgcca gcaagggaag cgagtcctgt 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccgga ttatggagaa 900
gtggatgatg aagttgaagt tcaaaaagaa gggaagatc tcgtgatcgc tttcaaccgg 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgcccacat gactggca 1098
```

<210> 144

Sequence_Listing_R10901_Corrected.txt

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
 1 5 10 15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
 20 25 30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
 35 40 45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
 50 55 60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
 65 70 75 80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
 85 90 95

Val Ile Ser Ser Gly Ser Thr Val Phe Arg Ile Thr Thr Met Pro Ala
 100 105 110

Asp Glu Phe Pro Glu Ile Thr Pro Ala Glu Ser Gly Ile Thr Phe Glu
 115 120 125

Val Asp Thr Ser Leu Leu Glu Glu Met Val Glu Lys Val Ile Phe Ala
 130 135 140

Ala Ala Lys Asp Glu Phe Met Arg Asn Leu Asn Gly Val Phe Trp Glu
 145 150 155 160

Leu His Lys Asn Leu Leu Arg Leu Val Ala Ser Asp Gly Phe Arg Leu
 165 170 175

Ala Leu Ala Glu Glu Gln Ile Glu Asn Glu Glu Glu Ala Ser Phe Leu
 180 185 190

Leu Ser Leu Lys Ser Met Lys Glu Val Gln Asn Val Leu Asp Asn Thr
 195 200 205

Thr Glu Pro Thr Ile Thr Val Arg Tyr Asp Gly Arg Arg Val Ser Leu
 210 215 220

Ser Thr Asn Asp Val Glu Thr Val Met Arg Val Val Asp Ala Glu Phe
 225 230 235 240

Pro Asp Tyr Lys Arg Val Ile Pro Glu Thr Phe Lys Thr Lys Val Val
 245 250 255

Val Ser Arg Lys Glu Leu Arg Glu Ser Leu Lys Arg Val Met Val Ile
 260 265 270

Ala Ser Lys Gly Ser Glu Ser Val Lys Phe Glu Ile Glu Glu Asn Val
 275 280 285

Sequence Listing_R10901_Corrected.txt

Met Arg Leu Val Ser Lys Ser Pro Asp Tyr Gly Glu Val Val Asp Glu
290 295 300

Val Glu Val Gln Lys Glu Gly Glu Asp Leu Val Ile Ala Phe Asn Pro
305 310 315 320

Lys Phe Ile Glu Asp Val Leu Lys His Ile Glu Thr Glu Glu Ile Glu
325 330 335

Met Asn Phe Val Asp Ser Thr Ser Pro Cys Gln Ile Asn Pro Leu Asp
340 345 350

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
355 360 365

<210> 145

<211> 972

<212> DNA

<213> *Thermatoga maritima*

<400> 145

```
atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
ctcctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
gatttcataa ggtctttact caggacaaag acgatctttt ccaacaagac gatcattgac 180
atcgtcaatt tcgatgagtg gaaagcacag gagcagaagc gtctcgttga acttttgaaa 240
aacgtaccgg aagacgttca tatcttcac cgttctcaaa aaacagggtg aaagggagta 300
gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
ttcagggaga atggtttgct catcgataaa gatgcccttc agctgttttt ctccaaggtt 420
ggaacgaacg acctgatcat agaaagggag attgaaaaac tgaaagctta ttccgaggac 480
agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540
gatgattttt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660
gatctcttca aaatcctcgt tcttgtgaca aagaaaagat actacacctg gcctgatgtg 720
tccaggggtg ccaaagagct gggaattccc gtctcctcgt tggctcgttt cctcggtttc 780
tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
gttagaaaag tactgagggg tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
agagatgaag aa 972
```

<210> 146

<211> 324

<212> PRT

<213> *Thermatoga maritima*

<400> 146

Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
1 5 10 15

Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
20 25 30

His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
35 40 45

Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
50 55 60

Sequence Listing_R10901_Corrected.txt

```

Asp Glu Trp Lys Ala Gln Glu Gln Lys Arg Leu Val Glu Leu Leu Lys
65          70          75          80
Asn Val Pro Glu Asp Val His Ile Phe Ile Arg Ser Gln Lys Thr Gly
85          90          95
Gly Lys Gly Val Ala Leu Glu Leu Pro Lys Pro Trp Glu Thr Asp Lys
100         105         110
Trp Leu Glu Trp Ile Glu Lys Arg Phe Arg Glu Asn Gly Leu Leu Ile
115         120         125
Asp Lys Asp Ala Leu Gln Leu Phe Phe Ser Lys Val Gly Thr Asn Asp
130         135         140
Leu Ile Ile Glu Arg Glu Ile Glu Lys Leu Lys Ala Tyr Ser Glu Asp
145         150         155         160
Arg Lys Ile Thr Val Glu Asp Val Glu Glu Val Val Phe Thr Tyr Gln
165         170         175
Thr Pro Gly Tyr Asp Asp Phe Cys Phe Ala Val Ser Glu Gly Lys Arg
180         185         190
Lys Leu Ala His Ser Leu Leu Ser Gln Leu Trp Lys Thr Thr Glu Ser
195         200         205
Val Val Ile Ala Thr Val Leu Ala Asn His Phe Leu Asp Leu Phe Lys
210         215         220
Ile Leu Val Leu Val Thr Lys Lys Arg Tyr Tyr Thr Trp Pro Asp Val
225         230         235         240
Ser Arg Val Ser Lys Glu Leu Gly Ile Pro Val Pro Arg Val Ala Arg
245         250         255
Phe Leu Gly Phe Ser Phe Lys Thr Trp Lys Phe Lys Val Met Asn His
260         265         270
Leu Leu Tyr Tyr Asp Val Lys Lys Val Arg Lys Ile Leu Arg Asp Leu
275         280         285
Tyr Asp Leu Asp Arg Ala Val Lys Ser Glu Glu Asp Pro Lys Pro Phe
290         295         300
Phe His Glu Phe Ile Glu Glu Val Ala Leu Asp Val Tyr Ser Leu Gln
305         310         315         320
Arg Asp Glu Glu

```

```

<210> 147
<211> 936
<212> DNA
<213> Thermatoga maritima

```

```

<400> 147
atgaacgatt tgatcagaaa gtacgctaaa gatcaactgg aaactttgaa aaggatcata 60

```

Sequence_Listing_R10901_Corrected.txt

```

gaaaagtctg aaggaatatc catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgttctg 180
gagatagatc ccgagggggg gaacataggc atagaagaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtaactga tagtccacga ctgtgaaaga 300
atgacccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgtc 360
gtgatcggtc tgaacactcg ccgttggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttgggt cggaaaaaact ttctggattg atggaaagtc tcaaagtttt ggagacggaa 600
aaactcttga aaaagggtct ttcaaaaggc ctccaagggt atctcgcatg tagggagctc 660
ctggagagat ttccaagggt ggaatogaag gaattctttg cgttttttga tcaggtgact 720
aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttcct cgattcaatt 840
ctcaggggtg agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936

```

<210> 148

<211> 312

<212> PRT

<213> *Thermatoga maritima*

<400> 148

```

Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
 1             5             10             15

Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
          20             25             30

Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
          35             40             45

Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
          50             55             60

Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
          65             70             75             80

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
          85             90             95

Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
          100            105            110

Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
          115            120            125

Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
          130            135            140

Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
          145            150            155            160

Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
          165            170            175

Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
          180            185            190

```

Sequence_Listing_R10901_Corrected.txt

```

Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
  195                                200                                205

Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
  210                                215                                220

Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
  225                                230                                235                                240

Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
  245                                250                                255

Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Gln Lys
  260                                265                                270

Ser Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu
  275                                280                                285

Asn Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg
  290                                295                                300

Lys Arg Gly Val Asn Ala Trp Ser
  305                                310

```

<210> 149
 <211> 423
 <212> DNA
 <213> *Thermatoga maritima*

```

<400> 149
atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
tacacgctca gcggaactcc agtcaccacc ttcaccatag cgggtggacag gggtcccaga 120
aagaacgcgc cggacgacgc tcaaacgact gatttcttca ggatcggtcac ctttggaaga 180
ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaaggtgaa 240
atgagaatga gaagatggga aacacccact ggagaaaaga gggatatctc ggaggttgtc 300
gcaaacgttg ttagattcat ggacagaaaa cctgctgaaa cagttagcga gactgaagag 360
gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420
ttt                                                                423

```

<210> 150
 <211> 141
 <212> PRT
 <213> *Thermatoga maritima*

```

<400> 150
Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
  1           5           10           15

Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
  20           25           30

Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
  35           40           45

Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
  50           55           60

```

Sequence_Listing_R10901_Corrected.txt

Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
65 70 75 80

Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
85 90 95

Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
100 105 110

Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
115 120 125

Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
130 135 140

<210> 151
<211> 1353
<212> DNA
<213> *Thermatoga maritima*

<400> 151
atgcgtgttc ccccgacaaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
gatccgtcgg taataaacga cgttccttgaa attttgagcc acgaagattt ctatctgaaa 120
aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180
gtggtttccg tctgtgacaa gcttcaaagc atgggaaaac tcgaggaagt aggtggagat 240
ctggaagtgg cccagctcgc tgaggctgtg cccagttctg cacacgcact tcactacgcg 300
gagatcgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgatc 420
ttcgagatct cagagatgaa aacgacaaaa tctacgatc atctgagagg catcatgcac 480
cgggtgtttg aaaacctgga gaacttcagc gaaagagcca acctataga acccggtgtg 540
ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600
agctccgatc tggtgataat agcagcgaga cctccatgg gaaaaacctc cttcgcactc 660
tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
atgtccaagg aacagctcgc tcaaagacta ctcagcatgg agtccggtgt ggatctttac 780
agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggcttct 840
aaactctaca aagcaccat agttgtggac gatgagtcac tctcgatcc gcgatcgtt 900
agggcaaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tgtcgactat 960
ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020
tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tggatgtagc gctttcacag 1080
ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140
tccggtgcga tagaacagga cgcagacaca gtcactctca tctacaggga ggaatattac 1200
aggagcaaaa aatccaaga ggaaagcaag cttcacgaac ctcacgaagc tgaaatcata 1260
ataggtaaac agagaaacgg tcccgttggc acgatcactc tgatcttcga cccagaacg 1320
gttacgttcc atgaagtcca tgtggtgcat tca 1353

<210> 152
<211> 451
<212> PRT
<213> *Thermatoga maritima*

<400> 152
Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
1 5 10 15

Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
20 25 30

Sequence_Listing_R10901_Corrected.txt

```

Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
    35                      40                      45

Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val
    50                      55                      60

Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp
    65                      70                      75                      80

Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala
                      85                      90                      95

Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu
    100                      105                      110

Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp
    115                      120                      125

Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser
    130                      135                      140

Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His
    145                      150                      155                      160

Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile
                      165                      170                      175

Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu
    180                      185                      190

Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala
    195                      200                      205

Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg
    210                      215                      220

Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu
    225                      230                      235                      240

Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly
                      245                      250                      255

Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp
    260                      265                      270

Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val
    275                      280                      285

Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala
    290                      295                      300

Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr
    305                      310                      315                      320

Leu Gln Leu Met His Leu Lys Gly Arg Lys Glu Ser Arg Gln Gln Glu
                      325                      330                      335

Ile Ser Glu Ile Ser Arg Ser Leu Lys Leu Leu Ala Arg Glu Leu Asp

```

Sequence_Listing_R10901_Corrected.txt

```

340                               345                               350
Ile Val Val Ile Ala Leu Ser Gln Leu Ser Arg Ala Val Glu Gln Arg
355                               360                               365

Glu Asp Lys Arg Pro Arg Leu Ser Asp Leu Arg Glu Ser Gly Ala Ile
370                               375                               380

Glu Gln Asp Ala Asp Thr Val Ile Phe Ile Tyr Arg Glu Glu Tyr Tyr
385                               390                               395                               400

Arg Ser Lys Lys Ser Lys Glu Glu Ser Lys Leu His Glu Pro His Glu
405                               410                               415

Ala Glu Ile Ile Ile Gly Lys Gln Arg Asn Gly Pro Val Gly Thr Ile
420                               425                               430

Thr Leu Ile Phe Asp Pro Arg Thr Val Thr Phe His Glu Val Asp Val
435                               440                               445

Val His Ser
450

```

<210> 153

<211> 1695

<212> DNA

<213> *Thermatoga maritima*

<400> 153

```

gtgattccctc gagagggtcat cgaggaaata aaagaaaagg ttgacatcgt agaggtcatt 60
tccgagtaacg tgaatccttac ccgggttaggt tccctcctaca gggctctctg tccctttcat 120
tcagaaacca atccttcttt ctacgttcat ccgggtttga agatatacca ttgtttcggc 180
tgcgggtgcga gtggagacgt catcaaattt cttcaagaaa tggaagggat cagtttccag 240
gaagcgctgg aaagacttgc caaaagagct gggattgatc tttctctcta cagaacagaa 300
gggacttctg aatacggaaa atacattcgt ttgtacgaag aaacgtggaa aaggtagctc 360
aaagagctgg agaaatcgaa agaggcaaaa gactatttaa aaagcagagg cttctctgaa 420
gaagatatag caaagttcgg ctttgggtac gtccccaaga gatccagcat ctctatagaa 480
gttgacagaag gcatgaacat aacactggaa gaacttgtca gatacggat cgcgctgaaa 540
aagggtgatc gattcgttga tagattcgaa ggaagaatcg ttgttccaat aaagaacgac 600
agtggtcata ttgtggcttt tgggtggcgt gctctcggca acgaagaacc gaagtatttg 660
aactctccag agaccaggtt tttttcgaag aagaagacc tttttctctt cgatgaggcg 720
aaaaaagtgg caaaagaggt tggtttttct gtcatcaccc aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgattcgg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaatec ctcgaggatc tctagacta cgaattcaac 960
gtgcttgtgg caaccccttc tcttacaaa gaccagatg aactctttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaac tcgcttctgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttctttga caggaacagc ccgcgggtg tgagatccta cttttctttc 1140
ctcaaaggtt gggctccaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg ttctatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaaggt ttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaac gcgaggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tctccaaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgcag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctcctcaga 1680
aaaataaaga ggagg
1695

```

Sequence_Listing_R10901_Corrected.txt

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

```

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
 1             5             10             15

Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
          20             25             30

Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
      35             40             45

Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
      50             55             60

Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
 65             70             75             80

Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
          85             90             95

Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
      100             105             110

Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
      115             120             125

Ala Lys Asp Tyr Leu Lys Ser Arg Gly Phe Ser Glu Glu Asp Ile Ala
      130             135             140

Lys Phe Gly Phe Gly Tyr Val Pro Lys Arg Ser Ser Ile Ser Ile Glu
      145             150             155             160

Val Ala Glu Gly Met Asn Ile Thr Leu Glu Glu Leu Val Arg Tyr Gly
          165             170             175

Ile Ala Leu Lys Lys Gly Asp Arg Phe Val Asp Arg Phe Glu Gly Arg
      180             185             190

Ile Val Val Pro Ile Lys Asn Asp Ser Gly His Ile Val Ala Phe Gly
      195             200             205

Gly Arg Ala Leu Gly Asn Glu Glu Pro Lys Tyr Leu Asn Ser Pro Glu
      210             215             220

Thr Arg Tyr Phe Ser Lys Lys Lys Thr Leu Phe Leu Phe Asp Glu Ala
      225             230             235             240

Lys Lys Val Ala Lys Glu Val Gly Phe Phe Val Ile Thr Glu Gly Tyr
          245             250             255

Phe Asp Ala Leu Ala Phe Arg Lys Asp Gly Ile Pro Thr Ala Val Ala
      260             265             270

```

Sequence_Listing_R10901_Corrected.txt

Val Leu Gly Ala Ser Leu Ser Arg Glu Ala Ile Leu Lys Leu Ser Ala
 275 280 285
 Tyr Ser Lys Asn Val Ile Leu Cys Phe Asp Asn Asp Lys Ala Gly Phe
 290 295 300
 Arg Ala Thr Leu Lys Ser Leu Glu Asp Leu Leu Asp Tyr Glu Phe Asn
 305 310 315 320
 Val Leu Val Ala Thr Pro Ser Pro Tyr Lys Asp Pro Asp Glu Leu Phe
 325 330 335
 Gln Lys Glu Gly Glu Gly Ser Leu Lys Lys Met Leu Lys Asn Ser Arg
 340 345 350
 Ser Phe Glu Tyr Phe Leu Val Thr Ala Gly Glu Val Phe Phe Asp Arg
 355 360 365
 Asn Ser Pro Ala Gly Val Arg Ser Tyr Leu Ser Phe Leu Lys Gly Trp
 370 375 380
 Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400
 Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415
 Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430
 Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445
 Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460
 Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480
 Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495
 Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510
 Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525
 Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540
 Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560
 Lys Ile Lys Arg Arg
 565

<210> 155

Sequence_Listing_R10901_Corrected.txt

<211> 804

<212> DNA

<213> Thermus thermophilus

<400> 155

```

atggctctac acccggtca cctggggca ataatcgggc acgaggccgt tctcgccctc 60
cttccccgcc tcaccgcca gacctgctc ttctccggcc ccgagggggg ggggcggcgc 120
accgtggccc gctggtacgc ctgggggctc aaccgcgggt tccccccgcc ctccctgggg 180
gagcaccogg acgtcctcga ggtggggccc aaggcccggg acctccgggg ccgggcccag 240
gtgcggctgg aggaggtggc gcccctcttg gagtgggtgt ccagccaccc ccgggagcgg 300
gtgaagggtg ccatacctgga ctgggcccac ctctcaaccg aggcgcgcgc caacgcccctc 360
ctcaaagctc tggaggagcc ccttcctac gcccgcatcg tctcctcgc cccaagccgc 420
gccaccctcc tccccaccct ggctcccg gccacggagg tggcattcgc ccccggtccc 480
gaggaggccc tgcgcgcct caccaggac ccggagctcc tccgctacgc cgcgggggcc 540
ccgggcccgc tcttagggc cctccaggac ccggaggggt accgggcccg catggccagg 600
gcgcaaaggg tctgaaagc cccgcccctg gacgcctcgt ctttgcttcg ggagcttttg 660
gccgaggagg agggggtcca cgcctccac gccgtcctaa agcgcgcgga gcacctcctt 720
gccctggagc gggcgcgga ggccctggag ggtacgtga gcccagagct ggtcctcgc 780
cggctggcct tagacttaga gaca                                     804

```

<210> 156

<211> 268

<212> PRT

<213> Thermus thermophilus

<400> 156

```

Met Ala Leu His Pro Ala His Pro Gly Ala Ile Ile Gly His Glu Ala
  1              5              10              15

Val Leu Ala Leu Leu Pro Arg Leu Thr Ala Gln Thr Leu Leu Phe Ser
      20              25              30

Gly Pro Glu Gly Val Gly Arg Arg Thr Val Ala Arg Trp Tyr Ala Trp
      35              40              45

Gly Leu Asn Arg Gly Phe Pro Pro Pro Ser Leu Gly Glu His Pro Asp
      50              55              60

Val Leu Glu Val Gly Pro Lys Ala Arg Asp Leu Arg Gly Arg Ala Glu
      65              70              75              80

Val Arg Leu Glu Glu Val Ala Pro Leu Leu Glu Trp Cys Ser Ser His
      85              90              95

Pro Arg Glu Arg Val Lys Val Ala Ile Leu Asp Ser Ala His Leu Leu
      100             105             110

Thr Glu Ala Ala Ala Asn Ala Leu Leu Lys Leu Leu Glu Glu Pro Pro
      115             120             125

Ser Tyr Ala Arg Ile Val Leu Ile Ala Pro Ser Arg Ala Thr Leu Leu
      130             135             140

Pro Thr Leu Ala Ser Arg Ala Thr Glu Val Ala Phe Ala Pro Val Pro
      145             150             155             160

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
      165             170             175

```

Sequence_Listing_R10901_Corrected.txt

Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
 180 185 190

Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
 195 200 205

Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
 210 215 220

Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
 225 230 235 240

Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
 245 250 255

Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
 260 265

<210> 157
 <211> 729
 <212> DNA
 <213> Thermus thermophilus

<400> 157
 atgctggacc tgagggaggt gggggaggcg gaggggaagg ccctaaagcc ccttttggaa 60
 agcgtgcccc agggcgtecc cgtcctctc ctggacccta agccaagccc ctcccggcg 120
 gcttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctgtg 180
 cggcacctgg aaaaccgggc caagcgctg gggctcaggc tcccgggcg ggtggcccag 240
 tacctggcct cctggaggg ggacctgag gccctggagc gggagctgga gaagcttgcc 300
 ctctctccc caccctcac cctggagaag gtggagaagg tggtagccct gagggcccc 360
 ctacagggt ttgacctggt gcgtccgtc ctggagaagg accccaagga ggccctcctg 420
 cgctaggcg gcctcaagga ggaggggag gagccctca ggtcctcgg ggcctctcc 480
 tggcagttc cctcctcgc cgggacctc ttctctctcc ggaaaaacc caggcccaag 540
 gaggaggac tcgcccgcct cgaggccac ccctacgcc cccgccgcg cctggaggcg 600
 gcgaagcgcc tcacggaaga ggccctcaag gaggcctgg acgcctcat ggaggggaa 660
 aagagggcca agggggggaa agaccctgg ctgcctctg aggcggcggt cctccgcctc 720
 gcccggtga 729

<210> 158
 <211> 292
 <212> PRT
 <213> Thermus thermophilus

<400> 158
 Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
 1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
 20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
 35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
 50 55 60

Sequence_Listing_R10901_Corrected.txt

```

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
65          70          75          80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
          85          90          95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
100          105          110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
115          120          125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
130          135          140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
145          150          155          160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
165          170          175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
180          185          190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
195          200          205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
210          215          220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
225          230          235          240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
245          250          255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260          265          270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275          280          285

Arg Leu Ala Arg
290

```

<210> 159

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 159

gtgtgtcata tgagtaagga ttctgtccac cttcacc

37

<210> 160

Sequence_Listing_R10901_Corrected.txt

```

<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat cgggggacta ctcggaagta aggg          34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtcata tggaaaccac aatattccag ttccag          36

<210> 162
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 162
gtgtgtggat ccttatccac catgagaagt atttttcac          39

<210> 163
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 163
gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g          41

<210> 164
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 164
gtgtgtggat ccttaatccg cctgaacggc taacg          35

```


Sequence_Listing_R10901_Corrected.txt

```

<210> 165
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 165
gtgtgtcata tgaactacgt tcccttcgcg agaaagtaca g          41

<210> 166
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 166
gtgtgtggat ccttaaaaca gctcgtccc gctgga          36

<210> 167
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 167
gtgtgtcata tgcgcgttaa ggtggacagg gag          33

<210> 168
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 168
tgtgtctcga gtcattggcta caccctcatt ggcatt          35

<210> 169
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 169
gtgtgtcata tgctcaataa ggtttttata ataggaagac ttacggg          47

```

Sequence_Listing_R10901_Corrected.txt

<210> 170
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt atttcgtcct ctteatcgg 39

<210> 171
<211> 807
<212> DNA
<213> Thermus thermophilus

<400> 171
atggtctgag gcctgaaccg cgttttcttc atcggcgccc tcgccaccgc gccggacatg 60
cgctacaccc cggcgggggt cgccattttg gacctgaccc tcgccgggtca ggacctgctt 120
cttttcgata acggggggga accggagggtg tcctgggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240
cgcttggagt accgccagtg ggaaagggag ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggacccccctg gacgaccggg ggaagaagcg gccggaggac agccggggcc 360
agcccaggct ccgcgcgcgc ctgaaccagg tcttctcat gggcaacctg acccgggacc 420
cggaactccg ctacaccccc cagggcaccc cggtggcccc gctgggcctg gcggtgaacg 480
agcgccgcca gggggcgag gagcgacccc acttcgtgga gggtcaggcc tggcgcgacc 540
tggcggagtg ggccgcccag ctgaggaagg gcgacggcct tttcgtgatc ggcaggttg 600
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccctg gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccgccgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> Thermus thermophilus

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45
Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu
50 55 60
Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly
65 70 75 80
Arg Leu Glu Tyr Arg Gln Trp Glu Arg Glu Gly Glu Lys Arg Ser Glu
85 90 95

Sequence_Listing_R10901_Corrected.txt

```

Leu Gln Ile Arg Ala Asp Phe Leu Asp Pro Leu Asp Asp Arg Gly Lys
    100                      105                      110

Lys Arg Ala Glu Asp Ser Arg Gly Gln Pro Arg Leu Arg Ala Ala Leu
    115                      120                      125

Asn Gln Val Phe Leu Met Gly Asn Leu Thr Arg Asp Pro Glu Leu Arg
    130                      135                      140

Tyr Thr Pro Gln Gly Thr Ala Val Ala Arg Leu Gly Leu Ala Val Asn
    145                      150                      155                      160

Glu Arg Arg Gln Gly Ala Glu Glu Arg Thr His Phe Val Glu Val Gln
    165                      170                      175

Ala Trp Arg Asp Leu Ala Glu Trp Ala Ala Glu Leu Arg Lys Gly Asp
    180                      185                      190

Gly Leu Phe Val Ile Gly Arg Leu Val Asn Asp Ser Trp Thr Ser Ser
    195                      200                      205

Ser Gly Glu Arg Arg Phe Gln Thr Arg Val Glu Ala Leu Arg Leu Glu
    210                      215                      220

Arg Pro Thr Arg Gly Pro Ala Gln Ala Cys Pro Gly Arg Arg Asn Arg
    225                      230                      235                      240

Ser Arg Glu Val Gln Thr Gly Gly Val Asp Ile Asp Glu Gly Leu Glu
    245                      250                      255

Asp Phe Pro Pro Glu Glu Asp Leu Pro Phe
    260                      265

```

<210> 173

<211> 992

<212> DNA

<213> Bacillus stearothermophilus

<400> 173

```

aattccgaca ttccaattga atcggtttatt ccgcttgaaa aagaaggcaa gttgctcggt 60
gatgtgaaaa gaccggggag catcgtagtg caggcgcgct tttctctga aatcgtagaa 120
aaactgccgc aacaaaacggg ggaatcgaa acggaagaca actttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaaacgccg acgaatatcc gcgcctgccg 240
caaattgaag aagaaaaagt gtttcaaato ccggctgatt tattgaaaac cgtgattcgg 300
caaacgggtg tcgccgtttc tacatcgga acgcgcccaa tcttgacagg tgtcaactgg 360
aaagttagaa atggcgagct tgtctgcaca gcgaccgaca gtcacgcgtt agccatgcgc 420
aaagtgaaaa ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttgatgac ggcaaccacc cggtagacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggtc gcttgacggc 600
aactatccgg agacggcccg cttgattcca acagaaaagca aaacgaccat gatcgtaact 660
gcaaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaa 720
aacgttgtga aactgacgac gcttctctga ggaatgctcg aaattttctc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgccggc gcttgatgga acagacattt 900
caaatcagct tcaactgggc catgcggccg ttcctgttgc gcccgcttca accgattcga 960
tgcttcagct cattttgcgc gtgagaacat at

```

Sequence_Listing_R10901_Corrected.txt

<210> 174

<211> 334

<212> PRT

<213> Bacillus stearothermophilus

<400> 174

Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
1 5 10 15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
20 25 30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
35 40 45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
50 55 60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
65 70 75 80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
85 90 95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
100 105 110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
115 120 125

Val Cys Thr Ala Thr Asp Ser His Arg Leu Ala Met Arg Lys Val Lys
130 135 140

Ile Ile Glu Ser Glu Asn Glu Val Ser Tyr Asn Val Val Ile Pro Gly
145 150 155 160

Lys Ser Leu Asn Glu Leu Ser Lys Ile Ile Leu Asp Asp Gly Asn His
165 170 175

Pro Val Asp Ile Val Met Thr Ala Asn Gln Val Leu Phe Lys Ala Glu
180 185 190

His Leu Leu Phe Phe Ser Arg Leu Leu Asp Gly Asn Tyr Pro Glu Thr
195 200 205

Ala Arg Leu Ile Pro Thr Glu Ser Lys Thr Thr Met Ile Val Asn Ala
210 215 220

Lys Glu Phe Leu Gln Ala Ile Asp Arg Ala Ser Leu Leu Ala Arg Glu
225 230 235 240

Gly Arg Asn Asn Val Val Lys Leu Thr Thr Leu Pro Gly Gly Met Leu
245 250 255

Glu Ile Ser Ser Ile Ser Pro Glu Ile Gly Lys Val Thr Glu Gln Leu
260 265 270

Gln Thr Glu Ser Leu Glu Gly Glu Glu Leu Asn Ile Ser Phe Ser Ala
275 280 285

Sequence_Listing_R10901_Corrected.txt

Lys Tyr Met Met Asp Ala Leu Arg Ala Leu Asp Gly Thr Asp Ile Gln
290 295 300

Ile Ser Phe Thr Gly Ala Met Arg Pro Phe Leu Leu Arg Pro Leu His
305 310 315 320

Thr Asp Ser Met Leu Gln Leu Ile Leu Pro Val Arg Thr Tyr
325 330

<210> 175

<211> 492

<212> DNA

<213> Bacillus stearothermophilus

<400> 175

atgattaacc ggcgcatttt ggctggcagg ttaacgagag atccggagtt gcgttacact 60
ccaagcggag tggctgttgc cacgtttacg ctccgggtca accgtccgtt tacaaatcag 120
cagggcgagc gggaaaacgga ttttattcaa tgtgtcgttt ggccgcgcca ggccgaaaac 180
gtcgccaact ttttgaaaaa ggggagcttg gctgggtgctg atggccgact gcaaaccgcg 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caattttcttg agccgaaagg aacgagcagc cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcag aaccaccaat atccgaacga aaaagggttt 420
ggccgcacat atgacgatcc tttcgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgccgt tt 492

<210> 176

<211> 164

<212> PRT

<213> Bacillus stearothermophilus

<400> 176

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
1 5 10 15

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
20 25 30

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
35 40 45

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
50 55 60

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
65 70 75 80

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
85 90 95

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
100 105 110

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
115 120 125

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp

Sequence_Listing_R10901_Corrected.txt

130

135

140

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
 145 150 155 160

Asp Leu Pro Phe

<210> 177

<211> 1044

<212> DNA

<213> Bacillus stearothermophilus

<400> 177

```

atgctggaac gcgatagggg aaacattgaa aaacggcggt tttctccctt ttatttatta 60
tacggcaatg agccgttttt attaacggaa acgtatgagc gatagggtgaa cgcagcgctt 120
ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180
gcgggcgcttg aggaggccga gacggtgccc tttttcggcg agcggcggtg cattctcatc 240
aagcatccat atttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
ctggaggcgt acttgaaggc gccgtgcgcg ttttcgatcg tcgtcttttt cgcgcggtac 360
gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420
atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
caagggggcg aagcaagcga cgaaggcatt gatgtcctgt tgcggcgggc cgggacgcag 540
ctttccgcct tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
atcgaggcgg cggcggttga gcggttctg gcccgcaacc cggaagaaaa cgtatttctg 660
cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
cttgaaaaaca atgaagagcc gatcaaaatt ttggcggttg tcgccgccca tttccgcttg 780
ctttcgcaag tgaaatggct tgcctcctta ggctacggac aggcgcaaat tgctgcggcg 840
ctcaaggtgc acccgttccg cgtcaagctc gctcttgctc aagcgggccc ctctcgctgac 900
ggagagcttg ctgaggcgat caacgagctc gctgaagcgc attacgaagt gaaaagcggg 960
gcggtcgatc gccggttggc cgttgagctg cttctgatgc gctggggcgc ccgcccggcg 1020
caagcggggc gccacggccg gcgg                                     1044

```

<210> 178

<211> 348

<212> PRT

<213> Bacillus stearothermophilus

<400> 178

Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
 1 5 10 15

Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
 20 25 30

Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
 35 40 45

Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
 50 55 60

Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile
 65 70 75 80

Lys His Pro Tyr Phe Phe Thr Ser Glu Lys Glu Lys Glu Ile Glu His
 85 90 95

Sequence_Listing_R10901_Corrected.txt

```

Asp Leu Ala Lys Leu Glu Ala Tyr Leu Lys Ala Pro Ser Pro Phe Ser
    100                      105                      110

Ile Val Val Phe Phe Ala Pro Tyr Glu Lys Leu Asp Glu Arg Lys Lys
    115                      120                      125

Ile Thr Lys Leu Ala Lys Glu Gln Ser Glu Val Val Ile Ala Ala Pro
    130                      135                      140

Leu Ala Glu Ala Glu Leu Arg Ala Trp Val Arg Arg Arg Ile Glu Ser
    145                      150                      155                      160

Gln Gly Ala Gln Ala Ser Asp Glu Ala Ile Asp Val Leu Leu Arg Arg
    165                      170                      175

Ala Gly Thr Gln Leu Ser Ala Leu Ala Asn Glu Ile Asp Lys Leu Ala
    180                      185                      190

Leu Phe Ala Gly Ser Gly Gly Thr Ile Glu Ala Ala Ala Val Glu Arg
    195                      200                      205

Leu Val Ala Arg Thr Pro Glu Glu Asn Val Phe Val Leu Val Glu Gln
    210                      215                      220

Val Ala Lys Arg Asp Ile Pro Ala Ala Leu Gln Thr Phe Tyr Asp Leu
    225                      230                      235                      240

Leu Glu Asn Asn Glu Glu Pro Ile Lys Ile Leu Ala Leu Leu Ala Ala
    245                      250                      255

His Phe Arg Leu Leu Ser Gln Val Lys Trp Leu Ala Ser Leu Gly Tyr
    260                      265                      270

Gly Gln Ala Gln Ile Ala Ala Ala Leu Lys Val His Pro Phe Arg Val
    275                      280                      285

Lys Leu Ala Leu Ala Gln Ala Ala Arg Phe Ala Asp Gly Glu Leu Ala
    290                      295                      300

Glu Ala Ile Asn Glu Leu Ala Asp Ala Asp Tyr Glu Val Lys Ser Gly
    305                      310                      315                      320

Ala Val Asp Arg Arg Leu Ala Val Glu Leu Leu Leu Met Arg Trp Gly
    325                      330                      335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
    340                      345

```

<210> 179

<211> 757

<212> DNA

<213> Bacillus stearothermophilus

<400> 179

```

atgcgatggg aacagctagc gaaacgccag ccggtggtgg cgaaaatgct gcaaagcggc 60
ttggaaaaag ggcggatttc tcatgcgtac ttgtttgagg ggcagcgggg gacgggcaaa 120
aaagcggcca gtttgttgtt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
ccgtgtctag agtgcgcgcaa ctgcgcggcg atcgactccg gcaaccaccc tgacgtccgg 240

```

Sequence_Listing_R10901_Corrected.txt

```

gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
ttctcgaaaa cagcgggtoga gtccgataaa aaaatgtaca tcgttgagca cgcgatcaa 360
atgacgacaa gcgctgccaa cagccttctg aaatttttgg aagagccgca tccggggacg 420
gtggcggtat tgctgactga gcaataccac cgctgtctag ggacgatcgt ttcccgtgt 480
caagtgcctt cgttcgggcc gttgccgcgc gcagagctcg cccagggact tgtcgaggag 540
cacgtgcctt tgccgttggc gctgttggct gccatttga caaacagctt cgaggaagca 600
ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgtttccg 720
cattttttgg aaagccatca gottgacctt ggacttg 757

```

<210> 180

<211> 252

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 180

```

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
 1           5           10           15

Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
          20          25          30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Leu Ala
          35          40          45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
          50          55          60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
          65          70          75          80

Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
          85          90          95

Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met
          100         105         110

Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser
          115         120         125

Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu
          130         135         140

Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys
          145         150         155         160

Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly
          165         170         175

Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His
          180         185         190

Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp
          195         200         205

Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly
          210         215         220

```


Sequence_Listing_R10901_Corrected.txt

Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro
225 230 235 240

His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu
245 250

<210> 181

<211> 1677

<212> DNA

<213> Bacillus stearothermophilus

<400> 181

```
gtggcatacc aagcgttata tcgctgtgtt cggccgcagc gctttgcgga catggtcggc 60
caagaacacg tgaccaagac gttgcaaagc gccctgcttc aacataaaat atcgcaacgt 120
tacttatttt ccggcccgcg cgggtacagga aaaacgagcg cagcgaaaat ttccgccaag 180
gcggtcaact gtgaacaggc gccagcgcg gagccatgca atgagtgtcc agcttgccctc 240
ggcattacga atggaacggt tcccgatgtg ctggaaattg acgctgcttc caacaaccgc 300
gtcgatgaaa ttcgtgatat ccgtgagaag gtgaaatttg cgcacaacgtc ggcccgctac 360
aaagtgtata tcacgcagca ggtgcataatg ctgtcgatcg gtgcgtttta cgcgctgttg 420
aaaacgttgg aggagcgcgc gaaacacgtc attttcattt tggccacgac cgagccgcac 480
aaaattccgg cgacgatcat tcccgcgtgc caacggttcg attttcgcgc catcccgtt 540
caggcgatcg tttaacggct aaagtacgtc gcaagcgccc aaggtgtcga ggctcagat 600
gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gctcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tcgacgacgt gctggcgatg 720
accggggctg catcatttgc cgccttatcg agcttcacgc aagccatcca ccgcaaagat 780
acagcggcgg ttcttcagca cttgaaaacg atgatggcg aagggaaga tccgcacgt 840
ttggttgaag acttgatttt gtaactatcg gatttattgc tgtacaaaac cgtccctat 900
gtggagggag cgattcaaat tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
attccggttt ccaatttata cgaggccatc gagttgctga acaaaagcca gcaagagatg 1020
aagtggacaa accaccgcgc ccttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080
tcagccgcgc ccccgctcgt gtccgcttcc gagttggaac cgttgataaa gcggattgaa 1140
acgctggagg cggaattgcg gcgcctgaag gaacaaccgc ctgcccctcc gtcgaccgcc 1200
gcgccggtga aaaaactgtc caaaccgatg aaaacggggg gatataaagc cccggttggc 1260
cgcatttacg agctgttgaa acaggcgacg catgaagatt tagctttggt gaaaggatgc 1320
tgggcggatg tgctcgacac gttgaaaacg cagcataaag tgcgcacgc tgccttgctg 1380
caagagagcg agccggttgc agcgagcgcc tcagcgttt tattaaaatt caaatacgaa 1440
atccactgca aaatggcgac cgatcccaca agttcgggtc aagaaaacgt cgaagcgatt 1500
ttgtttgagc tgacaaaccg ccgctttgaa atggtagcca ttccggaggg agaatgggga 1560
aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcgctgtgtt ggcaagagc tgatcgaat taaagaa 1677
```

<210> 182

<211> 559

<212> PRT

<213> Bacillus stearothermophilus

<400> 182

Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
1 5 10 15

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
20 25 30

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys

Sequence_Listing_R10901_Corrected.txt

50

55

60

Glu	Gln	Ala	Pro	Ala	Ala	Glu	Pro	Cys	Asn	Glu	Cys	Pro	Ala	Cys	Leu	65	70	75	80
Gly	Ile	Thr	Asn	Gly	Thr	Val	Pro	Asp	Val	Leu	Glu	Ile	Asp	Ala	Ala	85	90	95	
Ser	Asn	Asn	Arg	Val	Asp	Glu	Ile	Arg	Asp	Ile	Arg	Glu	Lys	Val	Lys	100	105	110	
Phe	Ala	Pro	Thr	Ser	Ala	Arg	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	115	120	125	
His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140	
Glu	Pro	Pro	Lys	His	Val	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His	145	150	155	160
Lys	Ile	Pro	Ala	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Arg	165	170	175	
Arg	Ile	Pro	Leu	Gln	Ala	Ile	Val	Ser	Arg	Leu	Lys	Tyr	Val	Ala	Ser	180	185	190	
Ala	Gln	Gly	Val	Glu	Ala	Ser	Asp	Glu	Ala	Leu	Ser	Ala	Ile	Ala	Arg	195	200	205	
Ala	Ala	Asp	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Leu	Leu	Asp	Gln	Ala	210	215	220	
Ile	Ser	Phe	Ser	Asp	Gly	Lys	Leu	Arg	Leu	Asp	Asp	Val	Leu	Ala	Met	225	230	235	240
Thr	Gly	Ala	Ala	Ser	Phe	Ala	Ala	Leu	Ser	Ser	Phe	Ile	Glu	Ala	Ile	245	250	255	
His	Arg	Lys	Asp	Thr	Ala	Ala	Val	Leu	Gln	His	Leu	Glu	Thr	Met	Met	260	265	270	
Ala	Gln	Gly	Lys	Asp	Pro	His	Arg	Leu	Val	Glu	Asp	Leu	Ile	Leu	Tyr	275	280	285	
Tyr	Arg	Asp	Leu	Leu	Leu	Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Glu	Gly	Ala	290	295	300	
Ile	Gln	Ile	Ala	Val	Val	Asp	Glu	Ala	Phe	Thr	Ser	Leu	Ser	Glu	Met	305	310	315	320
Ile	Pro	Val	Ser	Asn	Leu	Tyr	Glu	Ala	Ile	Glu	Leu	Leu	Asn	Lys	Ser	325	330	335	
Gln	Gln	Glu	Met	Lys	Trp	Thr	Asn	His	Pro	Arg	Leu	Leu	Leu	Glu	Val	340	345	350	
Ala	Leu	Val	Lys	Leu	Cys	His	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Ser	355	360	365	

Sequence_Listing_R10901_Corrected.txt

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380

Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400

Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415

Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430

Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445

Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460

Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480

Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495

Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510

Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525

Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540

Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183

<211> 4301

<212> DNA

<213> Bacillus stearothermophilus

<400> 183

atggtgacaa aagagcaaaa agagcggttt ctcacccctgc ttgagcagct gaagatgacg 60
 tcggacgaat ggatgccgca ttttcgtgag gcagccattc gcaaagtcgt gatcgataaa 120
 gaggagaaaa gctggcattt ttattttcag ttcgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgccgt ccgccatacg 240
 atggaggtcg aagcgccgcg cgtaactgag gcggatgtgc aggcgtattg gccgctttgc 300
 cttgccgagc tgcaagaagg catgtcgcgc cttgtcgatt ggctcagccg gcagacgcct 360
 gagctgaaag gaaacaagct gcttgtcgtt gcccgccatg aagcggaagc gctggcgatc 420
 aaacggcggg tcgccaaaaa aatcgctgat gtgtacgctt cgtttgggtt tccccccctt 480
 cagcttgacg tcagcgtcga gccgtccaag caagaaatgg aacagttttt ggcgcaaaaa 540
 cagcaagagg acgaagagcg agcgcttgct gtactgacgc atttagcgag ggaagaagaa 600
 aaggccgcgt ctgcgcgcgc gtccgggtccg cttgtcatcg gctatccgat ccgcgacgag 660
 gagccgggtgc ggcggttgga aacgatcgtc gaagaagagc ggcgcgctgt tgtgcaaggc 720
 tatgtatttg acgcgaagt gagcgaatta aaaagcggcc gcacgctgtt gaccatgaaa 780
 atcacagatt acacgaactc gatttttagtc aaaatgttct cgcgcgacaa agaggacgcc 840
 gagcttatga gcggcggtcaa aaaaggcatg tgggtgaaag tgcgcggcag cgtgcaaaac 900
 gatacgttcg tccgtgattt ggtcatcacc gccaacgatt tgaacgaaat cgcgcgcaaac 960

Sequence_Listing_R10901_Corrected.txt

```

gaacggcaag atacggcgcc ggaaggggaa aagaggggtcg agctccattt gcataccccg 1020
atgagccaaa tggacgcggt caccctcggtg acaaaaactca ttgagcaagc gaaaaaatgg 1080
gggcatccgg cgatcgccgt caccgaccat gccgttgttc agtcgtttcc ggaggcctac 1140
agcgcggcga aaaaacacgg catgaaggtc atttacggcc ttgaggcgaa catcgtcgac 1200
gatggcggtg cgatcgccct caatgagacg caccgcggtc ttctggagga aacgtacgtc 1260
gtctttgacg tcgagacgac gggcctgtcg gctgtgtaca atacgatcat tgagctggcg 1320
gcggtgaaag tgaagacgg cgagatcatc gaccgattca tgcgttttgc caacctgga 1380
catccgttgt cggtgacaac gatggagctg actgggatca ccgatgagat ggtgaaagac 1440
gccccgaagc cggacgaggt gctagcccggt tttgttgact gggccggcga tgcgacgctt 1500
gttggccaca acgccagctt tgacatcggt tttttaaacg cgggcctcgc tcgcatgggg 1560
cgcggaacaa tcgcgaatcc agtcacgtat acgctcgagc tggcccgttt tttatacccg 1620
gatttgaaaa caatcggtt caatacattg tgcaaaaaat ttgacattga attgacgcag 1680
catcaccggc ccatctacga cgcggaggcg accgggcatt tgcctatgcg gctgttgaag 1740
gaagcgggaag agcgcggcat actgtttcat gacgaattaa acagccgcac gcacagcgaa 1800
gcgtcctatc ggcttgccgc cccgttccat gtgacgctgt tggcgcaaaa cgagactgga 1860
ttgaaaaatt tgttcaagct tgtgtcattg tcgcacattc aatattttca ccgtgtgccc 1920
cgcacccggc gctccgtgct cgtcaagcac cgcgacggcc tgcctgtcgg ctccggctgc 1980
gacaaaggag agctgtttga caacttgatc caaaaggcgc cggagaagat cgaagacatc 2040
gcccgttttt acgattttct tgaagtgcac ccgcggagc tgtacaagcc gctcatcgag 2100
atggattatg tgaagacga agagatgac aaaaacatca tccgcagcat cgtcgccctt 2160
ggtgagaagc ttgacatccc ggttgtcgcc actggcaacg tccattactt gaaccagaaa 2220
gataaaattt accggaataa cttaatccat tcgcaaggcg gggcgaatcc gctcaaccgc 2280
catgaactgc cggatgtata tttccgtacg acgaatgaaa tgccttgactg cttctcgttt 2340
ttagggccgg aaaaagcgaa ggaaatcgtc gttgacaaca cgcaaaaaat cgcctcgtta 2400
atcggcgatg tcaagccgat caaagatgag ctgtatacgc cgcgcattga agggcgggac 2460
gaggaaatca gggaaatgag ctaccggcgg gcgaaggaaa tttacggcga cccgttgccc 2520
aaacttgttg aagagcggct tgagaaggag ctaaaaagca tcacggcca tggccttgcc 2580
gtcattttatt tgatctcgca caagcttggtg aaaaaatcgc tcgatgacgg ctacctgtc 2640
gggtcgcgcg gatcggtcgg ctcgctgttt gtcgcgacga tgacggaaat caccgaggtc 2700
aatccgctgc cgcgcatta cgtttgccc aactgcaagc attcggagtt ctttaacgac 2760
ggttcagtcg gctcagggtt tgatttgccc gataaaaact gccgcgatg tgggacgaaa 2820
tacaagaaag acgggcacga catcccgttt gagacgtttc tcggctttaa aggcgacaaa 2880
gtgcgggata tcgaacttgaa cttttccggc gaataccagc cgcgcgcccc caactatacg 2940
aaagtgtctg ttggcgaaga caacgtctac cgcgcgggga cgattggcac ggtcgctgac 3000
aaaacggcgt acggatttgt caaagcgtat gcgagcgacc ataacttaga gctgcgcggc 3060
gcggaaatcg acgctcgcg gctggctgca ccgggtgaa gcggacgacc gggcagcatc 3120
cggcgggcat catcgctgc cggattata tggaaattta cgattttacg ccgattcaat 3180
atcgggcca tgacacgtcc tctgaatggc ggacgaccca tttcgacttc cattcgatcc 3240
acgacaattt gttgaagctc gatattctcg ggcacgacga tccgacggtc attcgcatgc 3300
tgcaagattt aagcggcatc gatccgaaaa cgatcccgac cgacgacccg gatgtgatgg 3360
gcattttcag cagcaccgag ccgcttgccg ttacgcggga gcaaatcatg tgcaatgtcg 3420
gcacgatcgg cattccggag tttggcacgc gcttcgttcg gcaaatgttg gaagagacaa 3480
ggccaaaaac gttttccgaa ctcgtgcaaa tttccggctt gtcgcacggc accgatgtgt 3540
gctcggcga cgcgcaagag ctcatcmeta acggcacgtg tacgttatcg gaagtcacgc 3600
gtgcccga cgacattatg gtctatttga tttaccggcg gctcgagccg tcgctcgctt 3660
ttaaatcat ggaatccgtg cgcaaaggaa aaggcttaac gccggagttt gaagcagaaa 3720
tgcgcaaaaca tgacgtgccc gagtggtaca tcgatccatg caaaaaaatc aagtacatgt 3780
tcccgaaagc gcacgcccgc gcctacgtgt taatggcggt gcgcacggcc tactttaagg 3840
tgcaaccatc gcttttgtat tacgcgtcgt actttacggg gcggcgagg gactttgacc 3900
ttgacgcca gatcaaagga tcacccgcca ttcgcaagcg gattgaggaa atcaacgcca 3960
aaggcattca ggcgacggcg aaagaaaaaa gcttgctcac ggttccttag gtggccttag 4020
agatgtcgca gcgcggcctt tcctttaaaa atatcgattt gtaccgctcg caggcgacgg 4080
aattcgtcat tgadggcaat tctctcattc cgcggttcaa cgccattccg gggcttgagg 4140
cgaacgtggc gcaggcgatc gtgcgcgccc gcgaggaagg cgagtttttg tcgaaggagg 4200
atgtgcaaca gcgcggcaaa ttgtcgaaaa cgctgctcga gtatctagaa agcccgcggt 4260
gccttgactc gcttcagac cataaccagc tgcgctgtt t 4301

```

Sequence_Listing_R10901_Corrected.txt

<211> 1433

<212> PRT

<213> Bacillus stearothermophilus

<400> 184

```

Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
 1              5              10              15

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
      20              25              30

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
      35              40              45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
      50              55              60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
      65              70              75              80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
      85              90              95

Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
      100             105             110

Asp Trp Leu Ser Arg Gln Thr Pro Glu Leu Lys Gly Asn Lys Leu Leu
      115             120             125

Val Val Ala Arg His Glu Ala Glu Ala Leu Ala Ile Lys Arg Arg Phe
      130             135             140

Ala Lys Lys Ile Ala Asp Val Tyr Ala Ser Phe Gly Phe Pro Pro Leu
      145             150             155             160

Gln Leu Asp Val Ser Val Glu Pro Ser Lys Gln Glu Met Glu Gln Phe
      165             170             175

Leu Ala Gln Lys Gln Gln Glu Asp Glu Glu Arg Ala Leu Ala Val Leu
      180             185             190

Thr Asp Leu Ala Arg Glu Glu Glu Lys Ala Ala Ser Ala Pro Pro Ser
      195             200             205

Gly Pro Leu Val Ile Gly Tyr Pro Ile Arg Asp Glu Glu Pro Val Arg
      210             215             220

Arg Leu Glu Thr Ile Val Glu Glu Glu Arg Arg Val Val Val Gln Gly
      225             230             235             240

Tyr Val Phe Asp Ala Glu Val Ser Glu Leu Lys Ser Gly Arg Thr Leu
      245             250             255

Leu Thr Met Lys Ile Thr Asp Tyr Thr Asn Ser Ile Leu Val Lys Met
      260             265             270

Phe Ser Arg Asp Lys Glu Asp Ala Glu Leu Met Ser Gly Val Lys Lys
      275             280             285

```

Sequence_Listing_R10901_Corrected.txt

Gly	Met	Trp	Val	Lys	Val	Arg	Gly	Ser	Val	Gln	Asn	Asp	Thr	Phe	Val	290	295	300
Arg	Asp	Leu	Val	Ile	Ile	Ala	Asn	Asp	Leu	Asn	Glu	Ile	Ala	Ala	Asn	305	310	315
Glu	Arg	Gln	Asp	Thr	Ala	Pro	Glu	Gly	Glu	Lys	Arg	Val	Glu	Leu	His	325	330	335
Leu	His	Thr	Pro	Met	Ser	Gln	Met	Asp	Ala	Val	Thr	Ser	Val	Thr	Lys	340	345	350
Leu	Ile	Glu	Gln	Ala	Lys	Lys	Trp	Gly	His	Pro	Ala	Ile	Ala	Val	Thr	355	360	365
Asp	His	Ala	Val	Val	Gln	Ser	Phe	Pro	Glu	Ala	Tyr	Ser	Ala	Ala	Lys	370	375	380
Lys	His	Gly	Met	Lys	Val	Ile	Tyr	Gly	Leu	Glu	Ala	Asn	Ile	Val	Asp	385	390	395
Asp	Gly	Val	Pro	Ile	Ala	Tyr	Asn	Glu	Thr	His	Arg	Arg	Leu	Ser	Glu	405	410	415
Glu	Thr	Tyr	Val	Val	Phe	Asp	Val	Glu	Thr	Thr	Gly	Leu	Ser	Ala	Val	420	425	430
Tyr	Asn	Thr	Ile	Ile	Glu	Leu	Ala	Ala	Val	Lys	Val	Lys	Asp	Gly	Glu	435	440	445
Ile	Ile	Asp	Arg	Phe	Met	Ser	Phe	Ala	Asn	Pro	Gly	His	Pro	Leu	Ser	450	455	460
Val	Thr	Thr	Met	Glu	Leu	Thr	Gly	Ile	Thr	Asp	Glu	Met	Val	Lys	Asp	465	470	475
Ala	Pro	Lys	Pro	Asp	Glu	Val	Leu	Ala	Arg	Phe	Val	Asp	Trp	Ala	Gly	485	490	495
Asp	Ala	Thr	Leu	Val	Ala	His	Asn	Ala	Ser	Phe	Asp	Ile	Gly	Phe	Leu	500	505	510
Asn	Ala	Gly	Leu	Ala	Arg	Met	Gly	Arg	Gly	Lys	Ile	Ala	Asn	Pro	Val	515	520	525
Ile	Asp	Thr	Leu	Glu	Leu	Ala	Arg	Phe	Leu	Tyr	Pro	Asp	Leu	Lys	Asn	530	535	540
His	Arg	Leu	Asn	Thr	Leu	Cys	Lys	Lys	Phe	Asp	Ile	Glu	Leu	Thr	Gln	545	550	555
His	His	Arg	Ala	Ile	Tyr	Asp	Ala	Glu	Ala	Thr	Gly	His	Leu	Leu	Met	565	570	575
Arg	Leu	Leu	Lys	Glu	Ala	Glu	Glu	Arg	Gly	Ile	Leu	Phe	His	Asp	Glu	580	585	590
Leu	Asn	Ser	Arg	Thr	His	Ser	Glu	Ala	Ser	Tyr	Arg	Leu	Ala	Arg	Pro	595	600	605

Sequence_Listing_R10901_Corrected.txt

Phe His Val Thr Leu Leu Ala Gln Asn Glu Thr Gly Leu Lys Asn Leu
 610 615 620
 Phe Lys Leu Val Ser Leu Ser His Ile Gln Tyr Phe His Arg Val Pro
 625 630 635 640
 Arg Ile Pro Arg Ser Val Leu Val Lys His Arg Asp Gly Leu Leu Val
 645 650 655
 Gly Ser Gly Cys Asp Lys Gly Glu Leu Phe Asp Asn Leu Ile Gln Lys
 660 665 670
 Ala Pro Glu Glu Val Glu Asp Ile Ala Arg Phe Tyr Asp Phe Leu Glu
 675 680 685
 Val His Pro Pro Asp Val Tyr Lys Pro Leu Ile Glu Met Asp Tyr Val
 690 695 700
 Lys Asp Glu Glu Met Ile Lys Asn Ile Ile Arg Ser Ile Val Ala Leu
 705 710 715 720
 Gly Glu Lys Leu Asp Ile Pro Val Val Ala Thr Gly Asn Val His Tyr
 725 730 735
 Leu Asn Pro Glu Asp Lys Ile Tyr Arg Lys Ile Leu Ile His Ser Gln
 740 745 750
 Gly Gly Ala Asn Pro Leu Asn Arg His Glu Leu Pro Asp Val Tyr Phe
 755 760 765
 Arg Thr Thr Asn Glu Met Leu Asp Cys Phe Ser Phe Leu Gly Pro Glu
 770 775 780
 Lys Ala Lys Glu Ile Val Val Asp Asn Thr Gln Lys Ile Ala Ser Leu
 785 790 795 800
 Ile Gly Asp Val Lys Pro Ile Lys Asp Glu Leu Tyr Thr Pro Arg Ile
 805 810 815
 Glu Gly Ala Asp Glu Glu Ile Arg Glu Met Ser Tyr Arg Arg Ala Lys
 820 825 830
 Glu Ile Tyr Gly Asp Pro Leu Pro Lys Leu Val Glu Glu Arg Leu Glu
 835 840 845
 Lys Glu Leu Lys Ser Ile Ile Gly His Gly Phe Ala Val Ile Tyr Leu
 850 855 860
 Ile Ser His Lys Leu Val Lys Lys Ser Leu Asp Asp Gly Tyr Leu Val
 865 870 875 880
 Gly Ser Arg Gly Ser Val Gly Ser Ser Phe Val Ala Thr Met Thr Glu
 885 890 895
 Ile Thr Glu Val Asn Pro Leu Pro Pro His Tyr Val Cys Pro Asn Cys
 900 905 910
 Lys His Ser Glu Phe Phe Asn Asp Gly Ser Val Gly Ser Gly Phe Asp

Sequence_Listing_R10901_Corrected.txt

```

915                               920       925
Leu Pro Asp Lys Asn Cys Pro Arg Cys Gly Thr Lys Tyr Lys Lys Asp
 930                               935       940

Gly His Asp Ile Pro Phe Glu Thr Phe Leu Gly Phe Lys Gly Asp Lys
 945                               950       955       960

Val Pro Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Pro Arg Ala
          965                               970       975

His Asn Tyr Thr Lys Val Leu Phe Gly Glu Asp Asn Val Tyr Arg Ala
          980                               985       990

Gly Thr Ile Gly Thr Val Ala Asp Lys Thr Ala Tyr Gly Phe Val Lys
          995                               1000       1005

Ala Tyr Ala Ser Asp His Asn Leu Glu Leu Arg Gly Ala Glu Ile Asp
 1010                               1015       1020

Leu Ala Ala Gly Cys Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro
 1025                               1030       1035       1040

Gly Gly Ile Ile Val Val Pro Asp Tyr Met Glu Ile Tyr Asp Phe Thr
          1045                               1050       1055

Pro Ile Gln Tyr Pro Ala Asp Asp Thr Ser Ser Glu Trp Arg Thr Thr
          1060                               1065       1070

His Phe Asp Phe His Ser Ile His Asp Asn Leu Leu Lys Leu Asp Ile
          1075                               1080       1085

Leu Gly His Asp Asp Pro Thr Val Ile Arg Met Leu Gln Asp Leu Ser
          1090                               1095       1100

Gly Ile Asp Pro Lys Thr Ile Pro Thr Asp Asp Pro Asp Val Met Gly
 1105                               1110       1115       1120

Ile Phe Ser Ser Thr Glu Pro Leu Gly Val Thr Pro Glu Gln Ile Met
          1125                               1130       1135

Cys Asn Val Gly Thr Ile Gly Ile Pro Glu Phe Gly Thr Arg Phe Val
          1140                               1145       1150

Arg Gln Met Leu Glu Glu Thr Arg Pro Lys Thr Phe Ser Glu Leu Val
          1155                               1160       1165

Gln Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Gly Asn Ala
          1170                               1175       1180

Gln Glu Leu Ile Gln Asn Gly Thr Cys Thr Leu Ser Glu Val Ile Gly
 1185                               1190       1195       1200

Cys Arg Asp Asp Ile Met Val Tyr Leu Ile Tyr Arg Gly Leu Glu Pro
          1205                               1210       1215

Ser Leu Ala Phe Lys Ile Met Glu Ser Val Arg Lys Gly Lys Gly Leu
          1220                               1225       1230

```


Sequence_Listing_R10901_Corrected.txt

Thr Pro Glu Phe Glu Ala Glu Met Arg Lys His Asp Val Pro Glu Trp
1235 1240 1245

Tyr Ile Asp Ser Cys Lys Lys Ile Lys Tyr Met Phe Pro Lys Ala His
1250 1255 1260

Ala Ala Ala Tyr Val Leu Met Ala Val Arg Ile Ala Tyr Phe Lys Val
1265 1270 1275 1280

His His Pro Leu Leu Tyr Tyr Ala Ser Tyr Phe Thr Val Arg Ala Glu
1285 1290 1295

Asp Phe Asp Leu Asp Ala Met Ile Lys Gly Ser Pro Ala Ile Arg Lys
1300 1305 1310

Arg Ile Glu Glu Ile Asn Ala Lys Gly Ile Gln Ala Thr Ala Lys Glu
1315 1320 1325

Lys Ser Leu Leu Thr Val Leu Glu Val Ala Leu Glu Met Cys Glu Arg
1330 1335 1340

Gly Phe Ser Phe Lys Asn Ile Asp Leu Tyr Arg Ser Gln Ala Thr Glu
1345 1350 1355 1360

Phe Val Ile Asp Gly Asn Ser Leu Ile Pro Pro Phe Asn Ala Ile Pro
1365 1370 1375

Gly Leu Gly Thr Asn Val Ala Gln Ala Ile Val Arg Ala Arg Glu Glu
1380 1385 1390

Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
1425 1430

<210> 185

<211> 199

<212> PRT

<213> Thermus thermophilus

<400> 185

Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
1 5 10 15

Arg Leu Gly Leu Arg Leu Pro Gly Gly Val Ala Gln Tyr Leu Ala Ser
20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu

Sequence_Listing_R10901_Corrected.txt

```

65          70          75          80
Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
      85          90          95
Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
      100          105          110
Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
      115          120          125
Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
      130          135          140
Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
      145          150          155          160
Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys
      165          170          175
Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
      180          185          190
Ala Gly Gln Pro Arg Val Asp
      195

```

<210> 186
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 186
 gccacgtacc tcgcctccct cgagggg 27

<210> 187
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 187
 ggcccccttg gccttctcgg cctccat 27

<210> 188
 <211> 331
 <212> DNA
 <213> Thermus thermophilus

<400> 188
 agactcgagg ccctggagcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
 ctggagaagg tggagaaggt ggtggccctg agggccccc tcacgggctt tgacctggtg 120

Sequence_Listing_R10901_Corrected.txt

```
cgctccgtcc tggagaagga ccccaaggag gccctcctgc gccacaggcg cctcagggag 180
gaggggggagg agccccctcag gctcctcggg gccctctcct gccagttcgc cctcctcgcc 240
cgggccttct tctcctccg ggaaaacccc aggcccaagg aggaggacct cgcccgccctc 300
gaggcccacc cctacgccgc caagaaggcc a 331
```

<210> 189
 <211> 110
 <212> PRT
 <213> Thermus thermophilus

<400> 189
 Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
 1 5 10 15
 Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
 20 25 30
 Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
 35 40 45
 Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
 50 55 60
 Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
 65 70 75 80
 Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
 85 90 95
 Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
 100 105 110

<210> 190
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 190
 gtggtgtcta gacatcataa cggttctggc a 31

<210> 191
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR Primer

<400> 191
 gagggccacc accttctcca ccttctc 27

<210> 192

Sequence_Listing_R10901_Corrected.txt

```

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  PCR Primer

<400> 192
ctccgtcctg gagaaggacc ccaag                25

<210> 193
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  PCR primer

<220>
<221> primer_bind
<222> (15)
<223> S at position 15 can be either C or G

<220>
<221> primer_bind
<222> (27)
<223> S at position 27 can be either C or G

<400> 193
cgcggaattca acgcsctcct caagacsct          29

<210> 194
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  PCR primer

<400> 194
gacacttaac atatgggtcat cgccttcacc g        31

<210> 195
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  PCR primer

<400> 195
gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg  38

<210> 196
<211> 10

```

<212> PRT

<213> *Deinococcus radiodurans*

<400> 196

Val Ile Leu Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 197

<211> 10

<212> PRT

<213> *Methanococcus jannaschii*

<400> 197

Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 198

<211> 10

<212> PRT

<213> *Thermotoga maritima*

<400> 198

Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
1 5 10

<210> 199

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 199

ctggtgaacc cgggctccgt gggccagc

28

<210> 200

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 200

Leu Leu Val Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 201

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 201

ctcgaggagc ttgaggaggg tgttggc

27

<210> 202

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 202

Ala Asn Thr Leu Leu Lys Leu Leu Glu

1

5

<210> 203

<211> 32

<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser

1

5

10

15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly

20

25

30

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser

1

5

10

15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly

20

25

30

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser

1

5

10

15

Sequence_Listing_R10901_Corrected.txt

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
 20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
 1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
 20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggcccacc tcctcaccga 30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr
 1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccc cgtggagctc cac 33

Sequence_Listing_R10901_Corrected.txt

<210> 210
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: polypeptide

<400> 210
 Val Glu Leu His Ala Ala His Gly Tyr Leu Leu
 1 5 10

<210> 211
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 211
 ggctttccca tatggctcta caccggctc ac 32

<210> 212
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PCR primer

<400> 212
 gcgtggatcc acggtcatgt ctctaagtc 29